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OM protein - protein search, using sw model

Run on: February 14, 2005, 15:03:35 ; Search time 43 Seconds

(without alignments) 1458.915 Million cell updates/sec

Title: US-10-614-076-98
Perfect score: 3406

Sequence: 1 MNPNNRSEHDTIKVTPNSEL.....SFVSNKIVYDKEFIPVQL 652

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96226763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR70;*
1: PIR1;*
2: PIR2;*
3: PIR3;*
4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	2 139811	parasporal crystal
2	3222	94.3	659	2 S10228	parasporal crystal
3	2341.5	68.7	652	2 A27323	parasporal crystal
4	2125.2	63.2	649	1 JH0261	parasporal crystal
5	1122.5	33.1	1157	1 S49247	parasporal crystal
6	1124.5	33.0	719	2 I40590	cry465 Protein
7	1119	32.9	1138	2 A48944	parasporal crystal
8	1100.5	32.3	719	2 I39815	insecticidal prote
9	1091.5	32.0	719	2 I39814	insecticidal prote
10	1091.5	32.0	1228	2 S25383	parasporal crystal
11	1072.5	31.5	1160	2 S00873	parasporal crystal
12	1060	31.1	1160	2 I40589	parasporal crystal
13	963.5	28.3	1154	2 S39536	parasporal crystal
14	934.5	27.4	655	2 JC7140	protoxin - Bacillus
15	926.5	27.2	1189	2 S00914	parasporal crystal
16	907.5	26.6	823	2 S04181	parasporal crystal
17	906.5	26.6	1155	2 S02134	parasporal crystal
18	900.5	26.4	1155	2 A26513	parasporal crystal
19	899.5	26.4	1155	2 JD0002	parasporal crystal
20	899.5	26.4	1156	2 A29125	parasporal crystal
21	898.5	26.4	1174	2 A42459	parasporal crystal
22	895.5	26.3	1155	2 I39838	parasporal crystal
23	889.5	26.1	1181	2 A41052	parasporal crystal
24	886.5	26.0	1176	2 A48970	parasporal crystal
25	876	25.7	1176	2 JT0241	parasporal crystal
26	874	25.7	934	2 A22798	parasporal crystal
27	870	25.5	1176	2 JC2219	parasporal crystal
28	869.5	25.5	1171	2 I40572	parasporal crystal
29	869.5	25.5	1171	2 A37829	parasporal crystal

Result No.	Score	Query Match	Length	DB ID	Description
30	867.5	25.5	1177	2 A49785	parasporal crystal
31	867	25.5	1178	1 USBSXH	parasporal crystal
32	866.5	25.4	1166	2 S32645	parasporal crystal
33	866	25.4	1176	2 A22617	parasporal crystal
34	866	25.4	1176	2 S02115	parasporal crystal
35	861.5	25.3	618	2 S11445	parasporal crystal
36	845	24.8	1174	2 S32649	parasporal crystal
37	838.5	24.6	1165	2 S11446	parasporal crystal
38	828	24.3	1160	2 S32647	parasporal crystal
39	809	23.8	1156	2 A29938	parasporal crystal
40	787.5	23.1	1172	2 S32689	parasporal crystal
41	700	20.6	380	2 B42459	hypothetical prote
42	679	19.9	1156	2 S19106	parasporal crystal
43	665.5	19.5	1934	2 C29838	parasporal crystal
44	656.5	19.3	1136	1 USBSX1	parasporal crystal
45	637.5	18.7	1180	2 I39870	parasporal crystal
46	634.5	18.6	1180	2 A26558	mosquitocidal prot
47	482	14.2	613	2 JC6333	delta endotoxin -
48	279.5	8.2	1245	2 T18211	parasporal crystal
49	245.5	7.2	633	2 C32053	parasporal crystal
50	245	7.2	633	2 D32053	parasporal crystal
51	236	6.9	1385	2 T18213	parasporal crystal
52	233	6.8	262	2 A25140	parasporal crystal
53	228.5	6.7	1289	2 T18212	parasporal crystal
54	228	6.7	622	2 S17402	parasporal crystal
55	219.5	6.4	643	2 A43647	parasporal crystal
56	215.5	6.3	1186	2 T18210	parasporal crystal
57	138	4.1	904	2 G90563	lipoprotein [imp
58	129.5	3.8	2139	2 S46404	vitellogenin - yel
59	127.5	3.7	1513	2 S45768	mitotic spindle pr
60	126	3.7	937	2 C97168	glycosyltransferas
61	125.5	3.7	1193	2 S68218	botulinum neurotox
62	124	3.6	753	2 AG1710	maltosephosphoryla
63	121.5	3.6	1138	2 A82339	membrane nucleas
64	121.5	3.6	2529	2 B64635	toxin-like outer m
65	120.5	3.5	1133	2 JC4301	non-toxic-nonnemag
66	120	3.5	545	2 F86534	alpha-Glucosidase
67	119.5	3.5	835	2 E72305	hypothetical prote
68	119.5	3.5	1946	2 JC6332	lactocepain (EC 3.4
69	119	3.5	773	2 JE0387	exo-alpha-hisididas
70	119	3.5	1138	2 T18281	hypothetical prote
71	118	3.5	1127	2 T2817	ORF MSV156 hypoth
72	118	3.5	1285	2 S70582	botulinum neurotox
73	118	3.5	2166	2 G70163	hypothetical prote
74	117.5	3.4	753	2 A11339	maltosephosphoryla
75	117.5	3.4	2399	2 T18281	toxin-like outer m
76	117.5	3.4	4688	2 F82885	hypothetical prote
77	117	3.4	1175	2 F64489	hypothetical prote
78	117	3.4	2334	2 S32220	cell wall-associat
79	116.5	3.4	767	2 F71479	hypothetical prote
80	116	3.4	804	2 A53411	glucose-regulated
81	115.5	3.4	1276	2 S11455	botulinum neurotox
82	115	3.4	770	2 A11769	autolysin, amidase
83	115	3.4	802	2 A29517	endoplasmic reticu
84	114.5	3.4	376	2 A90206	histidinol-phospho
85	114.5	3.4	863	2 G98964	probable permease,
86	114.5	3.4	1193	2 G71605	hypothetical prote
87	114.5	3.4	1244	2 F90563	RAD2 endonuclease
88	114	3.4	713	1 A1BSG1	cyclomaltodextrin
89	114	3.4	803	2 A3554	probable peptidogl
90	114	3.4	925	2 D59105	hypothetical prote
91	114	3.4	1118	2 T28426	probable DNA direc
92	114	3.4	1407	2 S59823	probable membrane
93	114	3.4	1516	2 E71619	hypothetical prote
94	113.5	3.4	547	2 G69820	AMP-binding transp
95	113.5	3.4	1806	2 AF1717	hypothetical prote
96	113	3.4	644	2 T21137	hypothetical prote
97	113	3.4	749	2 T31536	hypothetical prote
98	113	3.4	1209	2 AH052	hypothetical prote
99	113	3.4	1477	2 T1534	probable tyrosine k
100	112.5	3.4	566	2 T50382	probable spindle p
101	112.5	3.4	2401	2 T28676	rioptry protein -
102	112	3.4	1375	2 S43375	hypothetical prote

103	111	3.3	1017	2	T18488	Query Match	100.0%	Score 3406; DB 2;	Length 652;
104	111	3.3	1067	2	T28663	Best Local Similarity	100.0%	Pred. No. 3..1e-20;	
105	111	3.3	1658	2	S5101	Matches 652; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
106	111	3.3	2910	2	T28156	Qy 1 MNPNRSEHDTIKTPNSLQTNHQYPLADPNPSTLKEFLRMTEDSSTEVLDS 60			
107	110.5	3.2	520	2	T18124	Db 1 MNPNRSEHDTIKTPNSLQTNHQYPLADPNPSTLKEFLRMTEDSSTEVLDS 60			
108	110.5	3.2	2485	1	H71622	Qy 61 TIVDAVGTQISINQGILGIVGDPFAGALTSEYQSFNLTWPSDADPKMAQVEVLIDK 120			
109	110	3.2	725	2	T19994	Db 61 TIVDAVGTQISINQGILGIVGDPFAGALTSEYQSFNLTWPSDADPKMAQVEVLIDK 120			
110	110	3.2	814	1	C40618	Qy 61 TIVDAVGTQISINQGILGIVGDPFAGALTSEYQSFNLTWPSDADPKMAQVEVLIDK 120			
111	110	3.2	1616	2	T16600	Db 61 TIVDAVGTQISINQGILGIVGDPFAGALTSEYQSFNLTWPSDADPKMAQVEVLIDK 120			
112	109.5	3.2	957	2	H97800	Qy 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
113	109.5	3.2	986	2	S30596	Db 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
114	109.5	3.2	1103	2	H92884	Qy 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
115	109.5	3.2	1119	2	B70126	Db 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
116	109	3.2	726	2	S62180	Qy 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
117	109	3.2	804	2	S51358	Db 121 KIEEYAKS KALAEQQLQNLNEDVYNAANSWKTKPLSRSKRSQRDIRELFSQAESHEPN 180			
118	109	3.2	1202	1	S03362	Qy 181 SMPSFAVSKPEVLFPTQAQANTHLLKIDAQVGEENGYSSSDVAFPYRQLKLTQY 240			
119	109	3.2	2819	2	A50551	Db 181 SMPSFAVSKPEVLFPTQAQANTHLLKIDAQVGEENGYSSSDVAFPYRQLKLTQY 240			
120	108.5	3.2	640	2	T0754	Qy 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
121	108.5	3.2	775	1	VPXRW6	Db 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
122	108.5	3.2	4450	2	U70340	Qy 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
123	108.5	3.2	4550	2	T18440	Db 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
124	108	3.2	593	2	F64523	Qy 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
125	108	3.2	851	2	S50670	Db 241 TDHCYNNWYNGNLNGRGSYDAWYKFNFRFREMTLTVIDLIVLFPFYDRLYSKGVKTEL 300			
126	108	3.2	986	2	H64459	Qy 301 TRDIFTDPIFSINTLQEQYGPTELSIENSTRKPHFLDYLQIGIEFHTRLQPGYFGKDSFNYW 360			
127	107.5	3.2	1086	2	T43266	Db 301 TRDIFTDPIFSINTLQEQYGPTELSIENSTRKPHFLDYLQIGIEFHTRLQPGYFGKDSFNYW 360			
128	107.5	3.2	1086	2	T02422	Qy 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
129	107.5	3.2	1468	1	S30818	Db 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
130	107.5	3.2	1790	1	S27772	Qy 361 SGNYVTRPIGSSKTTSPYGDKSTEPMQKLSFSDQYDQKNETSTQYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
131	107	3.1	300	2	T08453	Db 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
132	107	3.1	1048	2	H64459	Qy 361 SGNYVTRPIGSSKTTSPYGDKSTEPMQKLSFSDQYDQKNETSTQYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
133	107	3.1	1599	2	S22737	Db 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
134	107	3.1	2178	2	S55805	Qy 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
135	107	3.1	2364	2	T140884	Db 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
136	107	3.1	3262	2	AH2137	Qy 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
137	107	3.1	4196	2	T41274	Db 421 VTKYD7SOYDQNETSTOTYD5KRNNGHVAQDSD1DQLPPTDEPLEKAYSHQLYNAY 480			
138	106.5	3.1	822	2	BB2340	Qy 481 CPMQDRRGTRGTPFETWTHRSVDFNTIDAEK10LPVYKAYALSSGAS1IEGPGBTGGNL 540			
139	106.5	3.1	834	2	H64459	Db 481 CPMQDRRGTRGTPFETWTHRSVDFNTIDAEK10LPVYKAYALSSGAS1IEGPGBTGGNL 540			
140	106.5	3.1	891	2	G89357	Qy 481 CPMQDRRGTRGTPFETWTHRSVDFNTIDAEK10LPVYKAYALSSGAS1IEGPGBTGGNL 540			
141	106.5	3.1	945	2	A62714	Db 481 CPMQDRRGTRGTPFETWTHRSVDFNTIDAEK10LPVYKAYALSSGAS1IEGPGBTGGNL 540			
142	106.5	3.1	1272	2	S60999	Qy 541 LFLKESNS1AKFKYTLNSALLQYRVRIRYASTNLRLFVQNSNDLFLVYKNTMK 600			
143	106.5	3.1	1279	2	B64109	Db 541 LFLKESNS1AKFKYTLNSALLQYRVRIRYASTNLRLFVQNSNDLFLVYKNTMK 600			
144	106.5	3.1	1959	2	AG1085	Qy 541 LFLKESNS1AKFKYTLNSALLQYRVRIRYASTNLRLFVQNSNDLFLVYKNTMK 600			
145	106.5	3.1	4563	1	LPRUB	A;Title: Characterization of two genes encoding <i>Bacillus thuringiensis</i> insecticidal crys			
146	106	3.1	485	2	E70363	A;Reference number: 139811; MUID:9319147; PMID:1476436			
147	106	3.1	659	1	A62228	A;Status: preliminary; translated from GB/EMBL/DBJ			
148	106	3.1	1291	2	A49777	A;Molecule type: DNA			
149	106	3.1	1291	2	S46431	A;Residues: 1-652 <RES>			
150	106	3.1	2077	2	T44178	A;Cross-references: UNIPROT:P17969; EMBL:X17123; NID:940258; PMID:940259			

ALIGNMENTS

RESULT 2
S10228
parasporal crystal protein cry3Bal - *Bacillus thuringiensis* (fragment)
N;Alternate names: Coleopteran-active parasporal crystal protein; delta-a-endotoxin
C;Species: *Bacillus thuringiensis*
C;Accession: S10228
C;Date: 31-Dec-1993 #sequence_change 31-Dec-1993 #text_change 09-Jul-2004

R;Sick, A.; Gaertner, P.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A;Title: Sequence of a coleopteran-active toxin gene from a new isolate of *Bacillus thuringiensis* (fragment)
A;Reference number: S10228
A;Accession: S10228
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-59 <JC>
A;Gene: cryIIIB
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin; toxin
C;Genetics:

Query Match 94.3% Score 3212; DB 2; Length 659;
Best Local Similarity 93.7% Pred. No. 8.2e-198;
Matches 610; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

RESULT 1
I39811
Parasporal crystal protein cry3Bb1 - *Bacillus thuringiensis* (fragment)
C;Species: *Bacillus thuringiensis*
C;Accession: I39811
C;Date: 19-Jul-1996 #sequence_change 19-Jul-1996 #text_change 09-Jul-2004
R;Donovan, W.P.; Rupar, M.J.; Slaney, A.C.; Malvar, T.; Johnson, T.E.
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding *Bacillus thuringiensis* insecticidal crys

A;Reference number: 139811; MUID:9319147; PMID:1476436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-652 <RES>
A;Cross-references: UNIPROT:Q06117; GB:M89794; PID:9142730
C;Genetics:
C;Superfamily: cryIIIB2
C;Supfamily: parasporal crystal protein

Qy 1 MNPNRSEHTIKTPNSLQTNHNPYPLADNPNSTLLELNKERYFLRMTEDSSTEVLDS 60
 Db 9 MNPNRSEHTIKTPNSLQTNHNPYPLADNPNSTLLELNKERYFLRMTADNSTEVLS 68
 Qy 61 TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYOSFLNTWPSDADPKWKFMAQVEVLIDK 120
 Db 69 TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYOSFLNTWPSDADPKWKFMAQVEVLIDK 128
 Qy 121 KIEEYAKSKAKAELQGLQNPEDTYNALSWKCPPLSRSKRSQRDRLEFSQAESHRN 180
 Db 129 KIEEYAKSKAKAELQGLQNPEDTYNALSWKCPPLSRSKRSQRDRLEFSQAESHRN 188
 Qy 181 SMPSPAVSKPEVLFPLTYQAANTHLLIKDAQVGEETGYYSSSDVAEVYHROLKLTKQY 240
 Db 189 SMPSPAVSKPEVLFPLTYQAANTHLLIKDAQVGEETGYYSSSDVAEVYHROLKLTKQY 248
 Qy 241 TDHCVNWTWVGLNGLRGSTYDAWYKFNRFRRMELTLLVLIVLFPFYDRLYSKGVKVTL 300
 Db 249 TDHCVNWTWVGLNLSLRGSTYDAWYKFNRFRRMELTLLVLIVLFPFYDRLYSKGVKVTL 308
 Qy 301 TRDIFTDPFSLNTLQEXCPTFELSTNSRKPHFLDYLQGIEFHTRLQGPFYKSDPSNYW 360
 Db 309 TRDIFTDPFSLNTLQEXCPTFELSTNSRKPHFLDYLQGIEFHTRLQGPFYKSDPSNYW 368
 Qy 361 SGNYVETRSGSSKTTSPYGDKSTEVQKSLPQKSFQKVYRITANTDAWPNKGKVYLG 420
 Db 369 SGNYVETRSGSSKTTSPYGDKSTEVQKSLPQKSFQKVYRITANTDAWPNKGKVYLG 428
 Qy 421 VTKVDFSQYDDQNETSTQTYDSKRNNGHVSAQPSIDOLQPETTDEPLEKAYSHQLNAYE 480
 Db 429 VTKVDFSQYDDQNETSTQTYDSKRNNGHVSAQPSIDOLQPETTDEPLEKAYSHQLNAYE 488
 Qy 481 CFLMDQRRTSIPFPTWTHSVDFFNTIDELEKITOLPVVYKAYLSSGASIEGGFTGQNL 540
 Db 489 CFLMDQRRTSIPFPTWTHSVDFFNTIDELEKITOLPVVYKAYLSSGASIEGGFTGQNL 548
 Qy 541 LFLKESSNSIAKFTVTLNSALLORYRIVRYSTNLFLVQNSNNDELVINKTMK 600
 Db 549 LFLKESSNSIAKFTVTLNSALLORYRIVRYSTNLFLVQNSNNDELVINKTMN 608
 Qy 601 DDDITYQTDFLATTSNMGFSQGDNELITGAESFSNEKIVYDIEFIPVQ 651
 Db 609 DGDITYQTDFATTSNMGFSQGDNELITGAESFSNEKIVYDIEFIPVQ 659

RESULT 3
 A2 A27323
 parasporal crystal protein cry3Aa1 - *Bacillus thuringiensis*
 C;Species: *Bacillus thuringiensis*
 C;Accession: 19-Nov-1988 #sequence revision 19-Nov-1988 #text change 09-Jul-2004
 C;Accession: A27323; A26853; A29387; A28407; S60781; I399812; I39813
 R;Herrnstadt, C.; Gilroy, T.E.; Sobieski, D.A.; Bennett, B.D.; Gaertner, F.H.
 Gene 57, 37-46, 1987
 A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin
 A;Reference number: A27323; MUID:282880; PMID:282880
 A;Molecule type: DNA
 A;Residues: 1-652 <HER>
 A;Cross-references: UNIPROT:Q9S6N9; GB:M22472; NID:9142733; PID:9142734
 A;Experimental source: strain San Diego
 R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.
 A;Nucleic Acids Res. 15, 7183, 1987
 A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of *Bacillus thuringiensis*
 A;Reference number: A26853; MUID:3658680
 A;Molecule type: DNA
 A;Residues: 9-652 <HOE>
 A;Cross-references: GB:Y00420; NID:940252; PID:CAA68482.1; PMID:940253
 A;Experimental source: var. *tenebrionis*
 R;McPherson, S.A.; Perak, F.J.; Fuchs, R.U.; Marrone, P.G.; Lavrik, P.B.; Fischhoff, D.
 Bio/Technology 6, 61-66, 1988

A;Title: Characterization of the coleopteran-specific protein gene of *Bacillus thuringiensis*
 A;Reference number: A29987
 A;Accession: A29987
 A;Molecule type: DNA
 A;Residues: 9-652 <MCP>
 A;Experimental source: var. *tenebrionis*
 R;Bekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7056-7060, 1987
 A;Title: Molecular cloning and characterization of the insecticidal crystal protein gene
 A;Reference number: A28407
 A;Accession: A28407
 A;Molecule type: DNA
 A;Residues: 9-652 <SEK>
 A;Experimental source: var. *Tenebrionis*
 R;Adams, L.P.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.
 Mol. Microbiol. 14, 381-389, 1994
 A;Title: Elucidation of the mechanism of *CryIIA* overproduction in a mutagenized strain NB176, a mutant of strain NB176, a mutant of strain NB176
 A;Reference number: S60781; MUID:95131759; PMID:7830581
 A;Accession: S60781
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-652 <ADA>
 A;Cross-references: EMBL:U10985; NID:9506182; PID:943266.1; PID:95141312
 A;Experimental source: var. *Tenebrionis* strain NB176, a mutant of strain NB176
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
 R;Nu, S.J.; Dean, D.H.
 J. Mol. Biol. 255, 628-640, 1996
 A;Title: Functional significance of loops in the receptor binding domain of *Bacillus thuringiensis*
 A;Contents: annotation
 R;Donovan, W.P.; Gonzalez, J.M.
 Mol. Gen. Genet. 214, 365-372, 1988
 A;Title: Isolation and characterization of EG2158, a new strain of *Bacillus thuringiensis*
 A;Reference number: I39812; MUID:89112139; PMID:8568902
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 9-652 <RES>
 A;Cross-references: GB:M37207; NID:9142735; PID:9142736
 A;Experimental source: strain EG2158
 R;Reixeira De Souza, M.; Leclade, M.M.; Lereclus, D.
 J. Bacteriol. 175, 2932-2940, 1993
 A;Title: Full expression of the *CryIIA* toxin gene of *Bacillus thuringiensis* requires a regulatory element
 A;Reference number: I39813; MUID:93259939; PMID:8491716
 A;Accession: I39813
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 9-58 <RE2>
 A;Cross-references: GB:L03393; NID:9304150; PID:9551698
 C;Genetics:
 A;Gene: cryIIA
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin
 Query Match 68.7%; Score 2341.5; DB 2; Length 652;
 Best Local Similarity 68.6%; Pred. No. 4.2e-142; Mismatches 122; Indels 7; Gaps 6;
 Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;
 Qy 1 MNPNRSEHTIKTPNSLQTNHNPYPLADNPNSTLLELNKERYFLRMTEDSSTEVLDS 60
 Db 9 MNPNRSEHTIKTPNSLQTNHNPYPLADNPNSTLLELNKERYFLRMTADNSTEVLS 68
 Qy 61 TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYOSFLNTWPSDADPKWKFMAQVEVLIDK 120
 Db 69 TVKDAVGTGIVSIVGQILGVGVPPFAGALTFSYOSFLNTWPSDADPKWKFMAQVEVLIDK 128
 Qy 121 KIEEYAKSKAKAELQGLQNPEDTYNALSWKCPPLSRSKRSQRDRLEFSQAESHRN 180
 Db 129 KIEEYAKSKAKAELQGLQNPEDTYNALSWKCPPLSRSKRSQRDRLEFSQAESHRN 188
 Qy 181 SMPSEAVSKPEVLFPLPTYQAANTHLLIKDAQVEETGYYSSDVAEYHROLKLTKQY 240
 Db 188 SMPSEAVSKPEVLFPLPTYQAANTHLLIKDAQVEETGYYSSDVAEYHROLKLTKQY 247

Qy	241	TDHCUNWYNGLNGLGRSTYDAWKENRFRREMTLTVLDLIVLFFYDIRLYSRGVKTEL	300	Qy	301	TRDIFTDPISLNTLQEQYGPPTFLSIENSRXPHLFDYLOGIEFHTRLQPGYFGKDSFNYW	360					
Db	248	TDHCUNWYNGLNGLGRSTYDAWKENRFRREMTLTVLDLIVLFFYDIRLYSRGVKTEL	307	Db	298	TRDVLTPIVAVNNMNGYGTFSNQYKTYRPLDQYHQLQHFRPLQYFGCUDSFTNYW	357					
Qy	301	TRDIFTDPISLNTLQEQYGPPLSLENSIRXPHLFDYLOGIEFHTRLQPSFGKDSFNYW	360	Qy	361	SGNYVETRPSIGSSKTTISPFYGDKSTEPYQKLSFGQYKTYRPLDQYHQLQHFRPLQYFGCUDSFTNYW	416					
Db	308	TRDVLTPIVAVNNMNGYGTFSNQYKTYRPLDQYHQLQHFRPLQYFGCUDSFTNYW	367	Db	358	SGNYVTRSSSDETSIRSPFGNKTLDVNLEFFNGKTRAVANGNLAWPVGTTGCTK	417					
Qy	361	SGNYVETRPSIGSSKTTISPFYGDKSTEPYQKLSFGQYKTYRPLDQYHQLQHFRPLQYFGCUDSFTNYW	420	Qy	417	VILGTVTQDFSDQYDDQNETSTQYDQKRNHGHQSQSDIDQLPPTDDEPLKASHOL	476					
Qy	368	SGNYVTRPSIGSSKTTISPFYGDKSTEPYQKLSFGQYKTYRPLDQYHQLQHFRPLQYFGCUDSFTNYW	426	Db	418	IHSGYTKWQFSQYNDRDEVRLQTYDQSKRNGGI-YFVSDIDQLPPTDDEPLKASHOL	476					
Qy	421	VTKVDFSOYDDQNETSTQYDQKRNHGHQSQSDIDQLPPTDDEPLKASHOLNAYE	480	Qy	477	NTAECFIMQDRGTRTIPPTWTHRSVDFDNTIDAEXYKTOPLYVKAYALSSGASIIEGPGFT	536					
Db	427	VTKVDFSOYDDQNETSTQYDQKRNHGHQSQSDIDQLPPTDDEPLKASHOLNAYE	485	Db	477	NTVRCFELQIGGRRGTTIPPTWTHRSVDFDNTIDAEXYKTOPLYVKAYALSSGASIIEGPGFT	536					
Qy	481	CFLMQDRGRTIPPFETWTHRSVDFDNTIDAEXYKTOPLYVKAYALSSGASIILEGPGFTGGNL	540	Qy	537	GGNLFLPEKSSNSIAKFKVTLNSAALLQYRVRVIRYASTTNRLFVONSNNDFLVYINK	596					
Db	486	CFLMQDRGRTIPPFETWTHRSVDFDNTIDAEXYKTOPLYVKAYALSSGASIILEGPGFTGGNL	545	Db	537	GGDLIKCTNGS-GLTLYTTPAPDLYTKTYKIRYASTSQRFGDLSYTHSISYFDK	595					
Qy	541	LFLKESSNSIAKFKVTLNSAALLQYRVRVIRYASTTNRLFVQNSNNDFLVYINKTNMK	600	Qy	597	TMKDDDTYQTFDLATTNMNGFSGDKNELIGAESFSNEKTYDIEFIPV	650					
Db	546	IQCTE-NESSAATYVT-PDVSYSQYKTRHYASTSQTTFSLDQPAFQYQYFDXTINK	603	Db	596	TMDKGNTLTYNSFNLSSVSRIEISGG-NKIGSVGGGDEVYIDKIEFIPV	648					
Qy	601	DDDDITYQPFPLATTNMNGFSGDKNELIGAESFSNEKTYDIEFIPV	650	RESULT 5								
Db	604	GDTLTYNNSFLNLSFSTPPFELSG--NNLQIGVTGSLAQQYDQYKTYDIEFIPV	651	Qy	649247	parasporal crystal protein cry9c1 [validated] - Bacillus thuringiensis						
;Alternate names: parasporal crystal protein cry9C												
;Species: Bacillus thuringiensis												
;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004												
;Accession: A59350; S9247												
;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity against R;Lambert, B.; Bayse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; Vé												
parasporal crystal protein cry3c1 - Bacillus thuringiensis subsp. kurstaki (strain BT11) ;Name: parasporal crystal protein cry3c1												
;Species: Bacillus thuringiensis subsp. kurstaki												
;Accession: JH0261; S8944												
;Title: Nucleotide sequence of gene cry3c1 encoding a novel coleopteran-active crystal protein												
;Accession: JH0261; PMID:1544571												
;Accession: JH0261												
;Molecule type: DNA												
;Residues: 1-649 <LAM>												
;Cross-references: UNIPROT:Q45744; EMBL:X59797; PIDN:CAA42469-1; PID:940288												
;Genetics:												
;Gene: cry3c1												
;Superfamily: parasporal crystal protein												
;Query Match Score: 2152; DB 1; Length 649;												
;Best Local Similarity: 62.2%; Pred. No. 5, 60-130; Indels 10; Gaps 6;												
;Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;												
;Query Match Score: 2152; DB 1; Length 649;												
;Best Local Similarity: 62.2%; Pred. No. 5, 60-130; Indels 10; Gaps 6;												
;Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;												
Qy	1	MNPNNRSEHDHTIKVTPNSELQTNHNOYPLADNPNTNSTLLEFLNKFPLRMTEDSSTEVLDS	60	Qy	60	STV---KDAVGTGFSYVGQTLGVYGVPPAGALTSFYQSFLNITWP-SDADPWAFAAQV	114					
Db	59	TTKDAQKGISTIGDLYGFPYGGALVFTYNTWPLGQVEALIDQ	117	Db	60	PSLSISGRDAQTALTVGRIGLALQFSPQIVSEYQFLNTLMPVNNTDAIWEARMRQV	119					
Qy	121	KIEEYARKSALAELQGQNNPFDYNNALNSMKPLSLSKRSQDRIRLFSQAESHRN	180	Qy	115	EFLIDKIEEAKSKAELQGQNNPFDYNNALNSKTKPLSLSR-KRSQDRIRLFSQ	173					
Db	118	KIADYAKDKAQAEALQGQKFKDYSALSDWKTPLTLDGRSQDRIRLFSQAESHRN	177	Db	176	LDDPVDNAPLPAFVQVPLQSVYQAVNHLJLKDASHFEGWGFQGEISTYDRQ	235					
Qy	181	SMPSFAVSKFEVLFPLPYAQANTHLLKDAQVGEEMGYSSEDAVFYHQLKLQY	240	Qy	234	LKLTOQTDHCVNWWYNGLNGLGRSTYDAWVKNRFRREMTLTVLDLIVLFPYDRLY	293					
Db	178	SMPSFAVSKFEVLFPLPYAQANTHLLKDAQVGEEMGYSSEDAVFYHQLKLQY	237	Db	236	LEFTAKTNYCETWNTGDLRGTNTESWLRYHQPREMTLTVLDLIVLFPYDRLY	295					
Qy	241	TDHCUNWYNGLNGLGRSTYDAWVKNRFRREMTLTVLDLIVLFFYDIRLYSRGVKTEL	300	Qy	294	KGKTKTELTDRDIFP-----SLNTLQEXGP-----TFLSTENS-TRKPHLFDYLOGIEF	343					
Db	238	TNHCAYKTYAGLDRGTSYEWVKENRFRREMTLTVLDLIVLFFYDIRLYSRGVKTEL	297	Db	296	TGSNPOLTRVYDPIVNPANVGCLRRWGTNPNTFSELENAFRPRLPHDFDRNLSTI	355					

Qy	344 HTRLQPGYFGKDSFNYWGNVYETRPSIGSSKTTITSPFVY-----GDKSTEPVQ	391	Qy	344 HTRLQPGYFGKDSFNYWGNVYETRPSIGSSKTTITSPFVYGDKST-----EPVQKULSPDGOKVY	401
Db	356 SSNREP-----YSSNEDYWSQHTL-----RRSYNSDQSAQEDSYGLLITTRATTNPYDGTNRIE	411	Db	345 YELIS-----RSNTQYMNMMGCHRLRSPPIGALANSTQ-----GSTNTSINVY-TLQTSRVDY	399
Qy	392 KLSFDPGOKYRTTANTDVAAPNGKRYLQVYKVDQYDFSYQDQNETSTOTYDSKRNNNGHVS	451	Qy	402 RTIANTDVAAPNGKRYLQVYKVDQYDFSYQDQNETSTOTYDSKRNNNGHVS-----QDSID	457
Db	412 STAVDFRSALIGVYGNRASFVPGQFLNGTT-----SPANGGCRD	451	Db	400 RTPSLAGINLNLPTOPVN-GVPRVDF-----HWKEKPTLPASDNYXYLGAGVGTQLDQSEN	454
Qy	452 AODSIDQDLPETTDEPLEKAYSHOLNAYAECFLMDQR-----GTIPFETWTHRSVDF	504	Qy	458 QLPETTDEPLEKAYSHOLNAYAECFLMDQRGRTIPTFETWTHRSVDFPTIDARKITQLPV	517
Db	452 LYDNDLLEPDES-----TOSSTHAAUSHVFFFSRGTINQAGSIANAGSVTYWTRRDVDLN	507	Db	455 ELPETTGPNTYSESHRLSHGLISASHVKAHV-----YSWTHRSADRNTTIEPNSTQIPL	512
Qy	505 NTDAEKTOLPVKAYALSSGASLIEGGCPTGGNLLFLKESSNSIAKEFKTILNSAALLQ	564	Qy	518 VKAYALSSGASLIEGGCPTGGNLLFLKESSNSIAKEFKTILNSAALLQNYVRYASTN	577
Db	508 NTIPNPRITOLPVKAYASPVGRTVYLGKQGFTGGIL-----RRTTNGCTFGTRVTVNS-PLTQ	565	Db	513 VCAFNLSSGAAVYRGPGTGGDL-----RRTNTGFGDTRVMN-BPFAQYVRYVRYASTN	570
Qy	565 RYVRIRYASTTNRLFVONSNNDFLVYINKTMKDDDTYQTF-----DLATT-----NSNM	618	Qy	578 LRLEVQ-----NSNNDFLVYINKTMKDDDTYQTFDLATNSNMGFSGDKRNELIGA	631
Db	566 QYRLRVEFASTGNFSIRLVRGGSIGDVLRGSTMNRGQELTYESSFTREFTTGPENPPP	625	Db	571 LQHTSINGKAQNQN-----FSATMNMRGDEDLYKTFRTIGFTTGPENPPP	624
Qy	619 GFSGDQKNELJIGAESFVSNKEIYIDKIEFIPV	650	Qy	632 ESFVSNKEIYIDKIEFIPVOL	652
Db	626 TFTQAQEILTVNABGVSTGEYIYDRIEIPV	657	Db	625 WNFSSGNEVYIDRIEIPVVE	645
RESULT 6					
140590	CRYV465 protein - <i>Bacillus thuringiensis</i>		140590	CRYV465 protein - <i>Bacillus thuringiensis</i>	
C;Species: <i>Bacillus thuringiensis</i>			C;Species: <i>Bacillus thuringiensis</i>		
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004			C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004		
C;Accession: I40590			C;Accession: A48944		
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.			R;Lambert, B.; Hofte, H.; Anny, B.; Jangens, S.; Soetaert, P.; Peferoen, M.		
Appl. Environ. Microbiol. 61, 2432-2407, 1995			Appl. Environ. Microbiol. 58, 2536-2542, 1992		
A;Title: Distribution of cry-v-type insecticidal protein genes in <i>Bacillus thuringiensis</i> toncodius.			A;Title: Novel <i>Bacillus thuringiensis</i> insecticidal crystal protein with a silent activit		
A;Reference number: 133814; MUID:95314293; PMID:7793960			A;Reference number: A48944; MUID:92384571; PMID:1514800		
A;Status: preliminary; translated from GB/EMBL/DBJ			A;Contents: BTS137J		
A;Molecule type: DNA			A;Status: preliminary		
A;Residues: 1-719 <RES>			A;Molecule type: DNA; protein		
A;Cross-references: UNIPROT:Q45709; PIDN:9467234; PIDN:AAA82114.1; PID:94672			A;Residues: 1-1138 <LAM>		
C;Genetics:			A;Cross-references: UNIPROT:Q03749; GB: M64478; PIDN:9142760; PIDN:AAA22351.1; PID:9142761		
C;Gene: cryv465			A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIPI:112093)		
C;Superfamily: parasporal crystal protein			C;Superfamily: parasporal crystal protein		
RESULT 7					
A48944	parasporal crystal protein cryAA1 - <i>Bacillus thuringiensis</i>		A48944	parasporal crystal protein cryAA1 - <i>Bacillus thuringiensis</i>	
N;Alternate names: parasporal crystal protein cryAA1			N;Alternate names: parasporal crystal protein cryAA1		
C;Species: <i>Bacillus thuringiensis</i>			C;Species: <i>Bacillus thuringiensis</i>		
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004			C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004		
Matches 252; Conservative 135; Mismatches 223; Indels 65; Gaps 18;			Matches 251; Conservative 120; Mismatches 231; Indels 74; Gaps 19;		
Qy	1 MNPNNRSEHTDTI-----KVTPNSELQTNHNYQPLADNPNSTLEBLNKTKEFLRMTEDSSTEVIDNS	60	Qy	1 MNPNNRSEHTDTIKVTPNSELQTNHNYQPLADNPNSTLEBLNKTKEFLRMTEDSSTEVIDNS	60
Db	1 MKLKNPDKHQSLSSNAKVDIATDS-----LKNETDLEKNNNNEDVLRMSHE5	50	Db	1 MNLNNLDQYEDSNRTLNNSL-----NYPTQKALSPSLKMNQDFLSSTEREOPALASG	55
Qy	54 TEVDLNSTVKDAVTGIVSGQILGVGVGPAGALTSPYQSFTNTIWSDADWKAFA	113	Qy	61 TVKDAVTGIVSGQILGVGVGPAGALTSPYQSFTNTIWSDADWKAFAKMAVEVJDK	120
Db	51. --IDPFVYASSTIQTGIGAGKLTGQFAGQIAISLYSFLIGELWKGSQWEIMHE	107	Db	56 NT-AINTVQVSTGATISLGQGASPLTNTFLKAGLWPGNGKIDFMTVEEALDQ	113
Qy	114 VEILIDKKEEYAKSKAFLBQGQNLNPDDYNAVNLSPKTKPUSLRSRSQDIRELFSQ	173	Qy	121 KIEBEYAKSKAFLQNLNPDDYNAVNLNSW-----KTPPLSLASKRSQRDIRELFSQAESH	177
Db	108 VEEINQKILTYAARNLHILLRDSASLQDRLVYQHNSLESLEVY-----RNNTNTRARSVKNQY	164	Db	114 KIEBEYENKATAELDGLGSALDKYQKALADLGKQDPEATLSVATFRI-----IDSL	167
Qy	174 AESHFRNMSMPSEAVSKFEVTFPLPTYQAQANTHLLKQDQVGEENGYSSEDAEFYH	233	Qy	178 FRNSMPSPAVSKEFVLFPLPTYQAQANTHLLKQDQVGEENGYSSEDAEFYH	237
Db	165 LELMFVQKLPSPFASVGEVPLPPIYAQANLHILLRDSASLSTFVNQ	224	Db	168 FEFMSMPSFKVTFQYBIPPLTYQAQANTHLLKQDQVGEENGYSSEDAEFYH	227
Qy	224 LKLTOQYTHCWNWNGLNGLGSYDAMWVKENFRERMLTLDLIVLFPFYDYL	293	Qy	238 QOYTDDCVNWNVNGLNGLGSYDAMWVKENFRERMLTLDLIVLFPFYDYL	297
Db	225 VERTDYSHICMNTGNNLRTGNAWSWVQNFQKDTMLMVLDFLWPSYDITLVY	284	Db	228 SEYSDHCTKWNGLSLRSLNGSTEQWQINYNRPREMILMQLDQVAVPFHDPRRYSMETS	287
Qy	298 KGVTTELTDIIFDPIFSNLNTQYQEVYQPTPLSIEEN-SIRKPHLFYLOGIEFT-----RLQ	348	Db	288 TQLTREYVTDPVSLSNPDGSPSFQMENTAIRTPHLVYDLYTTSKYKAFSHEIQ	347
Db	285 IKTISQLREVYDAIGTHVPHNQAFASITWYNNNAPSFSAEAVRSPHLDFLKVTI	344			

Qy	343	FHTRLQGYFGKDSFNTYWSGNTYVETRPIGSSKTTISPFYGDCKSTEPEVQKLISFDGCKVYR 402
Db	344	IYSLLS-RWSNTQYMNNGGHKLEBFR-TIGTGNINISTQESTNTSINPV-TLPFTSDVYR 400
Qy	403	TIAINTDVAAPNGKVKVYGLVGTIVDFSOVDDQNETSTOTYDSKRNGH---VSAQDSIDQ 458
Db	404	TESLAGINLFLTQPVN-GPVPRDF---HWFKFTTHPIASDNFYPGYAGIGTQLODSENE 455
Qy	459	LPPEATTDEPLEKAYSHQNLNYAECFLMQDRRGTFPFTWTHRSYDFENTIDAEKITQLOPVV 518
Db	456	LPPEATCQNTYESYSHRLSHIGHLISASHVKALV-YSMWTHRSAAERTNTIEPNSNTOIPLV 513
Qy	519	KAYALSSGASITLBEQGPTGGNLLFLKBSSSNSTARFKTTLNSAAILQRYRVRIRYASTTNNL 578
Db	514	KAFNLISSGAAAVRGPGTGGDIL-RRNTGTFGDIKVNN-PPAQRQYRVRIRYASTTDL 571
Qy	579	RLFLVQ----NSNNDFLIVYINKTMKDDLYTQFTFLATTNSNMGFSDKNEILIGAE 632
Db	572	QFHTSINGKAQNQGN----FSATMNRGDEDLQYKTFRTVGFTTPSFUDVQSTETIGAW 625
Qy	633	SFVSNEKIXYDKEFPIFVQL 652
Db	626	NFSSGNNEVYDIEFVYVEV 645
RESULT 11		
Qy	500873	Parasporal crystal protein cryBai - <i>Bacillus thuringiensis</i> subsp. <i>thuringiensis</i>
C:	Alternate names: parasporal crystal protein cryA4	
C:	Species: <i>Bacillus thuringiensis</i> subsp. <i>thuringiensis</i>	
C:	Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004	
C:	Accession: S00873	
Qy	500873	Whiteley, H. R.
Db	500873	Nucleic Acids Res. 16, 273-274, 1988
A:	Title: Nucleotide sequence of an additional crystal protein gene cloned from <i>Bacillus thuringiensis</i> subsp. cryBai	
A:	Reference number: S00873; PMID:88023216; PMID:3362680	
A:	Accession: S00873	
A:	Molecule type: DNA	
A:	Residues: 1-1228 <BRI>	
A:	Cross-references: UNIPROT:PO5517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PIDN:CAA29898.1; PIDN:CAA29898.1	
C:	Genetics;	
A:	Gene: cryA4	
A:	Start codon: TTG	
C:	Superfamily: parasporal crystal protein	
C:	Keywords: delta-endotoxin	
Query Match Score 1072.5; DB 2; Length 1228;		
Best Local Similarity 36.6%; Pred. No. 1.7e-60; Matches 246; Conservative 120; Mismatches 27; Indels 59; Gaps 19;		
Qy	1	MNPNNRSEHDTDIKVTPNSELQTNHNNQYPLADNPNSTLBEILNYKEFLRMTEDSSTEVLQDN 60
Db	1	MTSNSRNENETTINAVSNHSAQMD-----LJDARTEDSCLCTAEGNN---IDPF 45
Qy	61	TVKDAVGTTGIVSGQIIGLVGVGVPGAGLTSFVQSFNLTWPSADPWAKFMAQVEVLIDK 120
Db	46	VSASTVQTGINIAGRILGVLGPGAGLASPFLVGPGRDQWIFLHEVQLINQ 105
Qy	121	KIEEYAKSKALAEQLOGIQLNNFDDYNNALNSWKKTPLSLRSKSQDRIRE-LFSQ---AES 176
Db	106	QITENARTAARLQGGDSPRAYQQLLEDWLS-----NRDARTTSVLYTQYIAEL 158
Qy	177	HFRNSMPSEAVSKFEEVFLPTYAQAAANTHLLKKDAQVGEENGYSSEDAEFPYHQLKL 236
Db	159	DFLNAMPFLFAIRNQEVPLMYYAQAAANHLLLRDASLGFSERGLTSQBIQYTERQVER 218
Qy	237	TQQTDTDHCYDNYVNGLNRSTYDAWVKFNFRMELTVLIVLEPPYDRLYSKV 296
Db	219	TRDYSDCYEVWNTGINSRLRTGNAASWVRYNQFRDITLGVLDDVLAQFSDRTPINT 278
Qy	297	KTELTRD1F7DPI-----FSLNTLQBYGPTFLSIE-NSIRKPHLFDYLOGLBFHTRLQ 348

Qy	380	PFYGDKSDEPVQKLSFDGOKVYR.-TIAINTDVAAPNGKVYLGVTKVDFSYQDDQKNETS	4.37
Db	385	RNTY-STATIVNYESENDRQVINTRSHTGL-GFQNAPLP-GITRAQF-----YP	4.32
Qy	438	TQTYDSKRNNGHYSQAQ--DSIDOLPPEPTEDEPLEKAYSHOLNAYAECFL-----MQDR	4.87
Db	433	GGTYSVTONALTQEQQNNSIDEPLOSSPNEP-SRSYSHRLSLTSITYHRLVLTIDGINY	4.92
Qy	488	RGTIPFETWTHRSVDFENTIDAAKITOLPUVKAYALSSGASLIELEGPGFTGGCNLFLKES	5.47
Db	493	SGNLPYTWTHRDYDLNTNTAARITOLPLVNSFEIAPGTTVVRGPGETGGDYL-RRTGV	5.51
Qy	548	NSTIAFKVTLNSALLQYRVRIRYASTTNRLFVQNSNNDFLIVYINKTMNDFDDDLTYQ	6.07
Db	552	GTGFTIRV-TRAPLQTQRIRRFASTTNLFGIRVGDROVNYFDGRTMNRGDELRYE	6.10
Qy	608	TFDLATINSNMGSGDKNEIITGAESFSNEKUYKIDKIEFIPV	6.50
Db	611	SEATRETFDTDNPROPEBLISVANANASAGOEVYTFDRREBIIIPV	6.53

RESULT 14
 JC7140 *Bacillus thuringiensis*
 Protoxin - *Bacillus thuringiensis*
 N:Alternate names: cryIC Protein
 C:Species: *Bacillus thuringiensis*
 C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C:Accession: JC7140
 R:Christov, N.K.; Imaishi, H.; Ohkawa, H.
 Biosci. Biotechnol. Biochem. 63, 1433-1444, 1999
 A:Title: Green-tissue-specific expression of a reconstructed cryIC gene encoding the actinopera litera.
 A:Reference number: JC7140; MUID:99430790; PMID:10501003
 A:Accession: JC7140
 A:Molecule type: DNA
 A:Residues: 1-655 <CHR>
 A:Cross-references: EMBL:X96682

A: Gene: cry1C
C: Superfamily: parasporal crystal protein
Genetics:

Query	Match	Score	Length
Qy	27.4%	934.5	DB 2;
Best Local Matches	Similarity	36.3%	Pred. No. 4.7e-52;
Matches	Conservative	103;	Mismatches 227;
Qy	21	QTNHNO--YPLADNPNSTLEELNYKEPLRMTBEDSSTEVLNDN--STYKDAVGTCISVG	74
Db	3	ENQNOCTPYNCISNPEVL--	42
Qy	75	QIIGUVGVYPAGLTSFVOSFLNTIWPSSADPKMKAQVEVILDKKIEEYAKSKAALEL	134
Db	43	QFLVSNPYPGGGLVGLDFVRCIVGPQQ--WDAFLVQIEQLINEAEEFARNAA,ANL	99
Qy	135	QGIQNNFEDYVNALNSWKKTPPLSLRSGRSQRDRIRELFSQAEHSFRNSMSPFAVSKFEVLF	194
Db	100	EGIIGNNFIYVVEPKWEEDP--NNPAATRTRYVDRFLDGLLERDIPSFRISGFEVPL	156
Qy	195	LPTYAOQANTHLLKDAQVFGGEWGYSSVEDAABFYHQLKLTQDHCYVWNYVNLNG	254
Db	157	LSVYQAQANLHLAIIIRDVIGFRWRGQDITINVENTANLRLIRHDEYADHCANTYNRGLANN	216
Qy	255	LRCSTYDAWKFNFRERMTLTVLDLIVLFPFDIIRLYSKGVTELTRDIFTDPIFLN-	313
Db	217	LPKSTYQDWITYNRLRRDTLTVLDIAAFFPNYDNRYPPIQPGVQLTREVYTDPLNFNP	276
Qy	314	TLCBYG--PTFLTIENS-IRKPBLFDYLGQIEFHTRLQPGYFGKDSFNYWSGNVETRPS	370
Db	277	QLQSVAQOLPTENMMESSAIRNPLHFDIILNLNTFT--DWFSVGRNFYWGHRVLS--S	330
Qy	371	IGSSKTTISPTSPFG--DKSTEPVQKLSFQDGKQYRTIANTDV--AAMPNGKYL-GYTKV	424
Db	331	LIGGGNTTSPYTCRANEOPPFRTFNG--PVERTLSPTRLQOOPPAPPNLRGYEGV	389

Qy	425	DFSYQDDQNETSTOTYDSKRNNGIVSAQDSIDQLPETTDEPLEKAYSHQUNYAEFCFLM	484
Db	390	EFS-----TPNTSTY--RGRGTV--DSLTTELPEPDNSVPPREGYSHRLCHA--TYP	434
Qy	485	QDRRGTTIP-----FTWTHRSVDPFTNTIDAEKITOLPVVKAYALSSGASITIEGPGFTCG	538
Db	435	VQRSCST-PFLTTGTVFWSWTHRSATNTIDPERINGQPLVKGFRWKGTSVITGPGFTCG	493
Qy	539	NLLFLKESSNSIAKPKVTLNSAALLQRYRIRYASTTNRLFV-----QNSNN	587
Db	494	DIL-RRNTGDFVSLQVNINS-PITQYRLRFYRASSDARVTLGQASTGGQSVN	551
Qy	588	DFLYIYINKTMNKODDLTYOTFDLATTNSNMGFS-----GDKNELLIGAESFVSNEKLY	641
Db	552	-----MPLQKTIMEIGENLTSRTFRYTDFSNPESFRANDIIGISEQQPGAGS-ISSGELY	606
Qy	642	IDKIEFI-648	
Db	607	IDKIEFI-613	

RESULT 15
 S00944 crystal protein crycal - *Bacillus thuringiensis* (strain entomocidus 60.5)
 parasporal crystal protein crycal - *Bacillus thuringiensis* (strain entomocidus 60.5)
 C.Species: *Bacillus thuringiensis*
 C.Date: 31-Dec-1990 #sequence_change 31-Dec-1990 #text_change 09-Jul-2004
 C.Accession: S00944
 R.Hone, G., van der Salm, T., Visser, B.
 Nucleic Acids Res. 16, 6240, 1988
 A.Title: Nucleotide sequence of crystal protein gene isolated from *B. thuringiensis* subsp. *israelensis*
 A.Reference number: S00944; MUID:88289380; PMID:3399402
 A.Accession: S00944
 A.Status: translation not shown
 A.Molecule type: DNA
 A.Residues: 1-1189 <HON>
 A.Cross-references: UNIPROT:P05518; EMBL:X07518; NID:940293; PID:CAA30396.1; PID:g402
 C.Superfamily: parasporal crystal protein
 C.Keywords: delta-endotoxin, *Bacillus*

Best Local Similarity	36.1%	Pred. No.	3..7e-11;	Indels	95;	Gaps	27;
Matches	241;	Conservative	103;	Mismatches	228;		
Qy	21	QTINHQ--YPLADNPNSTLLEBLNKEFLRMTEDSSTEVLDN--					
Db	3	ENNONQCIPYCNCLSNPEVU--					
Qy	75	QILGVVGYPPAGALTSPYQSFNLTIWPSDADPWAQFMAQYEVFLIDKKEEYAKSKALAEEL	134				
Db	43	QFLVSNFVPGGGFLVGLIDFWVGTVGPQS--WDAFLVQTEQLINERIAEAFRNAAAANL	99				
Qy	135	QGLQNNFEDDVNALNSWKRTPLSRSRSRSDRIRLFSQAESHHFRNMSPPSFAVSKFEVYL	194				
Db	100	EGLGNNNFIYVEAKFKEEDP--NNPPETRVDRFLDGLLERDIPSFRISGFEVPL	156				
Qy	195	LPTYAQAANTHLLKDAQYVGEEGYSSSDVAEPTYHTRLKLTQOYTDHCVNWNVYSLNG	254				
Db	157	LSTYQAQANLHLATLRSYHGLTINNEVYNNRLLRIDEADHCANTYRNGLN	216				
Qy	255	LRSSTYDAWKFNFRREMTLTVDLIVLPEFPYDRLYSSKGVKUTELTRDIDTPFISLN-	313				
Db	217	LPSSTYQDMITYNRLRDLTTLVDIAAFFPNYDNRYRPIOPVGQLTREVYTDPLINFP	276				
Qy	314	TQOBYG--PTFELSIENS-1RKPHLFDYLOGIEFHTRLQPGYFGKDSFNYWSGNYVETRPS	370				
Db	277	QLOSAQPTFNMESSRTRNPHLFIDLNLNTIFT--DWFESVGRNFYWGHRVIS--S	330				
Qy	371	IGSSKTTSPPYIG-DKSTEPVQKLSFGQKVRITANTDV--AARWPNKGKYL-GTKV	424				
Db	331	LIGGGNISPIYGEANQPPRSTFNG-PVFRPTLSPIPLLQQWPAPPENLRGYEGV	389				
Qy	425	DFSQYDDQKNETSTOTYDSKRNNGHVAQDSDIDOLPPTTDEPLEKAYSHOLNYAECFLM	484				

Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA--TF	434	Db	390	EFS-----TPTNSFTY--RGRGTV--DSLTELPPEDNSVPREGYSHRLCHA--TF	434
Qy	485	QDRRGTTIPF-----FTWTRSDPENTIAEKITOLPVKAYALSGASITIEPGPFITG	538	Qy	485	QDRRGTTIPF-----FTWTRSDPENTIAEKITOLPVKAYALSGASITIEPGPFITG	538
Db	435	VQRSGT-PEFLTGIVVPSWTDATLNTTIDPERINQIPLYKGFRWGGTSVTSVSPGFITG	493	Db	435	VQRSGT-PEFLTGIVVPSWTDATLNTTIDPERINQIPLYKGFRWGGTSVTSVSPGFITG	493
Qy	539	NLLFLKESSNSIAKPKVTLNSAALLQRYRIRYASTNTNRLFV-----QNSNN	587	Qy	539	NLLFLKESSNSIAKPKVTLNSAALLQRYRIRYASTNTNRLFV-----QNSNN	587
Qy	549	DIL-RRTNFGDFVSLQNNINS-PITQYRLRFRYASRDVTLGAASTGVGGQSVN	551	Db	494	DIL-RRTNFGDFVSLQNNINS-PITQYRLRFRYASRDVTLGAASTGVGGQSVN	551
Db	588	DLVLYIYINTKTMKDDDLTYQTFLATINSMGFS-----GDKNELLIGAESFVSNEKLY	641	Qy	588	DLVLYIYINTKTMKDDDLTYQTFLATINSMGFS-----GDKNELLIGAESFVSNEKLY	641
Qy	552	-MPLQKTMEEIGENITSRFRYTDTSNPFSSFRANPDILIGISEQPLFGAGS-ISSGELY	606	Db	552	-MPLQKTMEEIGENITSRFRYTDTSNPFSSFRANPDILIGISEQPLFGAGS-ISSGELY	606
Qy	642	IDKIEFI 648		Qy	642	IDKIEFI 648	
Db	607	IDKIEII 613		Db	607	IDKIEII 613	
RESULT 17							
	SO2134	parasporal crystal protein cryIC1 - <i>Bacillus thuringiensis</i> (strain aizawai IC1)					
		N;Alternate names: delta-endotoxin					
		C;Species: <i>Bacillus thuringiensis</i>					
		C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004					
		C;Accession: SO1481					
		C;Accession: S012134; #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004					
		C;Accession: S012134; #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004					
		R;Haider, M.Z.; Ellar, D.J.					
		Mol. Microbiol. 3, 229-238, 1989					
		A;Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda delta-endotoxin					
		A;Reference number: S04181; PMID:89343627; PMID:3205732					
		A;Accession: S04181					
		A;Molecule type: DNA					
		A;Residues: 1-823 <SAN>					
		A;Cross-references: UNIPROT:P05518; EMBL:X13620; NID:940355; PID:CAA31951.1; PID:940356					
		A;Gene: bta					
		C;Superfamily: parasporal crystal protein					
		C;Keywords: delta-endotoxin					
Query Match							
Qy	21	QTNHNO--YPLADNPNSTLNEYKEPLRMTEDSSTEVLDN--STVKAATGTTGIVSVVG	74	Qy	21	QTNHNO--YPLADNPNSTLNEYKEPLRMTEDSSTEVLDN--STVKAATGTTGIVSVVG	74
Db	3	ENNONQCFCYNCISNPPEVIL-----LDGERISTGNSSIDISLVL-	42	Db	3	ENNONQCFCYNCISNPPEVIL-----LDGERISTGNSSIDISLVL-	42
Qy	75	QILGVGVGVFAGALTSTYFCOSFLNTIWPSDADPKAFMAQVEVILDKKIEYAKSKALAEI	134	Qy	75	QILGVGVGVFAGALTSTYFCOSFLNTIWPSDADPKAFMAQVEVILDKKIEYAKSKALAEI	134
Db	43	QFLVSNFVGFGVGLIDEFWGIVGPSSO--WDAFLVQIEQLINERAFPARNAIAANL	99	Db	43	QFLVSNFVGFGVGLIDEFWGIVGPSSO--WDAFLVQIEQLINERAFPARNAIAANL	99
Qy	135	QGLONNFEKYVNALNSWKTPLSLRSKESDRLFQQAEHSFRNEMPSFAVSKFIVL	194	Qy	135	QGLONNFEKYVNALNSWKTPLSLRSKESDRLFQQAEHSFRNEMPSFAVSKFIVL	194
Db	100	EGLGNMNFNTYVEAFKEWEDP--NNPATRTRVDRFLGILERDPIPSISGFEPVL	156	Db	100	EGLGNMNFNTYVEAFKEWEDP--NNPATRTRVDRFLGILERDPIPSISGFEPVL	156
Qy	195	LPTVQAQANTHLLIKDAVQFGEWGVYSSVEDVAEYFHRQLKTQQYDTHCNWNYGLNG	254	Qy	195	LPTVQAQANTHLLIKDAVQFGEWGVYSSVEDVAEYFHRQLKTQQYDTHCNWNYGLNG	254
Db	157	LSVYQAQANLHLAIRDSVTFGERWLITINVNENYNLRHDEYADHCANTYRNGLNN	216	Db	157	LSVYQAQANLHLAIRDSVTFGERWLITINVNENYNLRHDEYADHCANTYRNGLNN	216
Qy	255	LRGSTYDAWVYKTFNFRFREMLTVLDIRVYPPFDYLGQIEFTRLQGYFDGKDFSDENWGNVYETRPS	370	Qy	255	LRGSTYDAWVYKTFNFRFREMLTVLDIRVYPPFDYLGQIEFTRLQGYFDGKDFSDENWGNVYETRPS	370
Db	217	LPKSTYQDNNTYNRRLDTLTVLDDIAAFTPNRRFPIQPYGQLTREVYDPLINFP	330	Db	217	LPKSTYQDNNTYNRRLDTLTVLDDIAAFTPNRRFPIQPYGQLTREVYDPLINFP	330
Qy	314	TLOQEYG-PPFLSLENS-TRKPHLFDYLGQIEFTRLQGYFDGKDFSDENWGNVYETRPS	370	Qy	314	TLOQEYG-PPFLSLENS-TRKPHLFDYLGQIEFTRLQGYFDGKDFSDENWGNVYETRPS	370
Db	277	QLQSYAQLPFLVNMENNSAARNPHLFDIIMNLNTIPT--DWFSYGRNFTWGGHHRVIS-	330	Db	277	QLQSYAQLPFLVNMENNSAARNPHLFDIIMNLNTIPT--DWFSYGRNFTWGGHHRVIS-	330
Qy	371	IGSSKTTSPFYG-DKSTPBPVQKLSFDGGQKVYRT-TANTDVAAPWNGKVYL--GVTKV	424	Qy	371	IGSSKTTSPFYG-DKSTPBPVQKLSFDGGQKVYRT-TANTDVAAPWNGKVYL--GVTKV	424
Db	331	LIGGENITSPYGRANQEPRSFTFNG-PVFRTISIPIPTLQCPHFLNRLRGGGV	389	Db	331	LIGGENITSPYGRANQEPRSFTFNG-PVFRTISIPIPTLQCPHFLNRLRGGGV	389
Qy	425	DFSQYDDQKNETSTQYDSKRKNNGHVSQAQSDIDOLPPETDEPLEKAYSHOLNYAECFLM	484	Qy	425	DFSQYDDQKNETSTQYDSKRKNNGHVSQAQSDIDOLPPETDEPLEKAYSHOLNYAECFLM	484
Db	224	RDWIRYNOFRRELTTVLDIVSLFNPYDSDRTYPIRTVSOLTRTEYTNPV---LENFDG	278	Db	224	RDWIRYNOFRRELTTVLDIVSLFNPYDSDRTYPIRTVSOLTRTEYTNPV---LENFDG	278

Qy	321 TP----LSIENSIRKPHLFDYLOGIEFHTRLQPGYFGKUDSFNTWSGNVTETRPSIGSSRT 376	Db	333 FTFPLYGTGMNAAQFQRIAVQLGGCVYRTLSS-----LYRPFNIGINNQQLSVL 383
Db	279 SFRGSAQGEGSIRSPLHMDILNSITIYDAHREY----YWSGHQIMASPVGFSGPE 332	Qy	430 DDQKNETSTQ-----YDSKRNGHVSQDSDTDLQPLPPTTDEPLKAYSHOLNAYABCFL 483
Qy	377 ITSPFYGDK-STEPVQKLSFD-GQKVYRINTDVAAPNGKTY----LGVTKVDPSQY 429	Db	384 DGTEFAYGTSSNLPSAVY---RISGTV---DSLDIBPQNQNNYPROGFSHRLSHVSMFR 437
Db	333 FTFPLYGMNAAPQCRIVAQQLGCVYRTLSS-----LYRPFNIGINNQQLSVL 383	Qy	484 MQDRRTI-----PFPTMTHRSVDFNTIDAEKITQLPVKAYALSSGASITEGGFTGG 538
Qy	430 DDQKNETSTQ-----YDSKRNGHVSQDSDTDLQPLPPTTDEPLKAYSHOLNAYABCFL 483	Db	438 SGFNNSSVIIIRAPMFSWIRSAEFPNNIIPSSQ.TQIPLKSTNLGSQTSSVVKGPFTGG 497
Db	384 DGTEFAYGTSSNLPSAVY---RISGTV---DSLDIBPQNQNNYPROGFSHRLSHVSMFR 437	Qy	539 NLFLKESSNSIAKFKYTLLNSAALQRYRVRVRYASTTNLRLFQ-----NSNNDLFLV 592
Qy	484 MQDRRTI-----PFPTMTHRSVDFNTIDAEKITQLPVKAYALSSGASITEGGFTGG 538	Db	498 DIL-RRTSGQISITLVRN1-TAPLSQRVRYRVASTTNLQFHTSIDGRPINQGN-----550
Db	438 SGFNNSSVIIIRAPMFSWIRSAEFPNNIIPSSQ.TQIPLKSTNLGSQTSSVVKGPFTGG 497	Qy	593 YINKTMNKKDDDTYQTFDLATTSNMGSGDKNEELIGAESFSVNEKLYIDKEFIPVQL 652
Qy	539 NLFLKESSNSIAKFKYTLLNSAALQRYRVRVRYASTTNLRLF-----VONSNNDFLVI 592	Db	551 -FSATMSSSNLQSGSFRTVGFITPFENPSNGSSVFTLSAHVFNSGNEYVDRTEPVPAEV 609
Db	498 DIL-RRTSGQISITLVRN1-TAPLSQRVRYRVASTTNLQFHTSIDGRPINQGN-----550		
Qy	593 YINKTMNKKDDDTYQTFDLATTSNMGSGDKNEELIGAESFSVNEKLYIDKEFIPVQL 652		RESULT 19
Db	551 -FSATMSSSNLQSGSFRTVGFITPFENPSNGSSVFTLSAHVFNSGNEYVDRTEPVPAEV 609		
		JD0002	parasporal crystal protein cytLab3 - <i>Bacillus thuringiensis</i> parasporal crystal protein delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein
		C:Species: Bacillus thuringiensis	C:Species: <i>Bacillus thuringiensis</i>
		C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 09-Jul-2004	C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
		C:Accession: A90025; A91560; A90955; S14555; A6461; A24172; A29043; JD0002	C:Accession: A90025; A91560; A90955; S14555; A6461; A24172; A29043; JD0002
		R;Kondo, S.; Tamura, N.; Kunitate, A.; Akashi, A.; Ohmori, I.	R;Kondo, S.; Tamura, N.; Kunitate, A.; Akashi, A.; Ohmori, I.
		A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i>	A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i>
		A;Reference: A90025	A;Reference: A90025
		A;Molecule type: mRNA	A;Molecule type: mRNA
		A;Residues: 1-1155 <KON>	A;Residues: 1-1155 <KON>
		A;Cross-references: UNIPROT:P06578	A;Cross-references: UNIPROT:P06578
		A;Experimental source: subsp. kurstaki	A;Experimental source: subsp. kurstaki
		R;Geiser, M.; Schweizer, S.; Grimm, C.	R;Geiser, M.; Schweizer, S.; Grimm, C.
		A;Title: The hyper-variable region in the genes coding for entomopathogenic crystal protein	A;Title: The hyper-variable region in the genes coding for entomopathogenic crystal protein
		A;Reference number: A91560; MUID:87163505; PMID:3557124	A;Reference number: A91560; MUID:87163505; PMID:3557124
		A;Accession: A91560	A;Accession: A91560
		A;Molecule type: DNA	A;Molecule type: DNA
		A;Residues: 1-1155 <GET>	A;Residues: 1-1155 <GET>
		A;Cross-references: GB: M15271; NID:9143123; PIDN:AAA22561.1; PID:9143124	A;Cross-references: GB: M15271; NID:9143123; PIDN:AAA22561.1; PID:9143124
		A;Experimental source: subsp. kurstaki	A;Experimental source: subsp. kurstaki
		R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.	R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
		DNA 5, 305-314, 1986	DNA 5, 305-314, 1986
		A;Title: <i>Bacillus thuringiensis</i> entomocidal protoxin sequence and gene product analysis	A;Title: <i>Bacillus thuringiensis</i> entomocidal protoxin sequence and gene product analysis
		A;Reference number: A90955; MUID:8630092; PMID:3743328	A;Reference number: A90955; MUID:8630092; PMID:3743328
		A;Accession: A9055	A;Accession: A9055
		A;Molecule type: DNA	A;Molecule type: DNA
		A;Residues: 1-1155 <WAB>	A;Residues: 1-1155 <WAB>
		A;Cross-references: GB: M13898; NID:9142719; PIDN:AAA22330.1; PID:9142720	A;Cross-references: GB: M13898; NID:9142719; PIDN:AAA22330.1; PID:9142720
Db	54 AG----FVGLVLDIWIQGPQ---WDFFLYQEQLINQRLEEFARNQAIISRLGSLNL 106	Db	54 AG----FVGLVLDIWIQGPQ---WDFFLYQEQLINQRLEEFARNQAIISRLGSLNL 106
Qy	141 FEDVNAALSWKKTPLSLSKRSDRIRELFSQAESHRNMSMPSFAVSKFEVFLPLTYA 200	Db	107 YQIYAEASPEWEADPTN_PALREEMRIQ_FNMDSNALTIAFLAVQNYQPLLSVRYQ 163
Qy	3 NNPIN-ECIPIY---NCIUSNPVEVLLGBERIE---TGYPTDLSITQFULSEFVPG 53	Db	201 AANTHLLIJKDAQVFGEEGVYSSDVAEYFHROLKLTKQYDHCVNNTVYGLRGSY 260
Qy	85 AGATLSPYQSFNLNTW----PSDADPWFKAQVEVLLDKKIREYAKSKALABQLGLON 140	Db	164 AANLHLSVRLDVSFGQRGFDAATINSYNDLTLRIGNTDHARWNTGJLWRWGDD 223
Db	54 AG----FVGLVLDIWIQGPQ---WDFFLYQEQLINQRLEEFARNQAIISRLGSLNL 106	Qy	261 DANYKFNPRRPREMLTIVLFLIVLFFPYDYLRLSKGVKTELTDIPTBPSLNTLQEQGP 320
Qy	141 FEDVNAALSWKKTPLSLSKRSDRIRELFSQAESHRNMSMPSFAVSKFEVFLPLTYA 200	Db	224 RDWTRYNQFRELLTIVLVLIVSFLPNYDSTRTYPIRTVSQLTRELYTNPV----LENFDG 278
Qy	31 DNPNISTLEFLNQYKFRLMTEDSSTEVTNLSVTKDAVNGTISVVG-----QIIGVGVCP 84	Db	321 TPLS----JENSIRKPHLFDYLOGIEFHTRLQPGYFGKUDSFNTWSGNVTETRPSIGSSRT 376
Db	3 NNPIN-ECIPIY---NCIUSNPVEVLLGBERIE---TGYPTDLSITQFULSEFVPG 53	Qy	279 SFRGSAQGEGSIRSPLHMDILNSITIYDAHREY----YWSGHQIMASPVGFSGPE 332
Qy	261 DANYKFNPRRPREMLTIVLFLIVLFFPYDYLRLSKGVKTELTDIPTBPSLNTLQEQGP 320	Db	377 ITSPFYGDK-STEPVQKLSFD-GQKVYRINTDVAAPNGKTY----LGVTKVDPSQY 429
		Qy	C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

Qy	822	VPFAGALTSPYQSPUNLIVPSDADEWKAQMAQVEVLIDKKEEYAKSKALABEGLQLNQN 141	Db	107	YQIYAESPREEADPTN - PALREBMRIQ - ENDINNSALTTAIPLFAVQNYQVPLLSVYQ 163
Db	49	VPGIVAFQIFLDLWGFITPSD -- -WSELLQIQLIERIETLERNRITTURGLADSY 105	Qy	201	AANTHLLIKDAQVGFEEWGSSEDAVEPHRQLKLTQOYTDHCVNTWVNGLNGRSTY 260
Qy	142	EDYVNALNSWKKTKPLSLRSKRSQDRIRELFSQAFSHFRNSMPSFAVSKFEVLFLPTYQA 201	Db	164	AANLHLISVLRDVSVFQWKGFDAATINSRNDLTLRIGHNTDHAWRINTGLERVWGPDS 223
Db	106	EYIEARRWEANP -- -NNAQLRDEVRTRFANTDDALITAINNFTLTSEIPLLSVYQA 162	Qy	261	DANVKFNREREMTTLVLDLIVLFPYDYLRSKGVKTBTRDIFTDPIFSLATLQEYGP 320
Qy	202	ANTHLLIKDAQVGFEEWGSSEDAVEPHRQLKLTQOYTDHCVNTWVNGLNGRSTY 261	Db	224	RDWIRYNQFRRELTLVLDLIVSLPLNPNSRSTYPRTVSOLTEYTNPY --- LENFDG 278
Db	163	ANHLHLISVLRDVSVFQWKGFDAATINSRNDLTLRIGHNTDHAWRINTGLERVWGPDS 222	Qy	321	TF --- -LSIENSIRKPHLFDYLOGIEFHTRLQPSYFGKDSFNYWSGNVETRPSIGSSKT 376
Qy	262	AWVKENREREMTTLVLDLIVLFPYDYLRSKGVKTBTRDIFTDPIFSLATLQEYGP 321	Db	279	SFRGAAQGTEGSIRSPhMIDLNSITIYDAHGEY --- -YWSGHQIMASPGFSGDPE 332
Db	223	QWAFNQFRRELTLVLDLIVLFPYDYLRSKGVKTBTRDIFTDPIFSLATLQEYGP 321	Qy	377	ITSPPYQGDK - STEPVKQLSFD - GQKYKTTIANTDVAAPNGKQY --- - LGVTKVDFSQY 429
Qy	322	-FUSIENSIRKPHLFDYLOGIEFHTRLQPSYFGKDSFNYWSGNVETRPSIGSSKT 376	Db	333	FTPFLYGTMGNAAPQQRIVAOULGQGVRTLSST --- -LYRPPFNGINNNQQLSVL 383
Db	283	GFMRAEFGVYRPHLMDFMMSL - FVTAETRSQ --- - - - - - TWGHLVYSSRNATAGN - R 330	Qy	430	DDQKNETSTQT --- -YDSKRNGHVSQDSDIDQLPPPTTDSSPLKAYSHQLNAYAECP 483
Qy	377	ITSPPYQGDK - STEPVKQLSFD - GQKYKTTIANTDVAAPNGKQY --- - LGVTKVDFSQY 429	Db	384	DGTEFAYGTSSNPLPSAVY --- -RKGSTV --- -DSLDEIPOPNNNVPPRGQFSHRLSHVSMFR 437
Db	331	INFPSYGVFNPGGAIWIADEDPRP --- - - - - - FYRTLSDPVFVRGSGFNPYVGLGR 380	Qy	484	MQDRRTGI --- -PFETPTWHSYDFDENTIDAEKITQPLPVVKAYALLSSGASIIEGPQFTG 538
Qy	424	VDPFQYQDDDKNETSTQYDQSKRNGHVSQDSDIDQLPPPTTDEPLEXAYSHQLNAYAECP - 482	Db	438	SFGNSNSVSIIRAPMFSWVHRSANFNNIIPSSQITQIPLKSTNLGSGTSVVKPGPFTG 497
Db	381	VAFQQ --- - - - - - TGTNHTHTFRNSTI --- -DSLDEIPOPDNSGAAPNDYSHVLNHVTFR 430	Qy	539	NLFLPKKESSNSIAKPKTYTNSAALLQYRVRTRIYASTNLRFLPVQ --- -NSNNDFLVYI 592
Qy	483	--- -LMQDERRGTIPFPTWTHRSYDFDENTIDAEKITQPLPVVKAYALLSSGASIIEGPQFTG 538	Db	498	DIL - RRTSPGQISSLTRVNI - TAPLSQYRTRVTRIYASTNLRFLQFTSIHGRPINQCN --- 550
Db	431	WPGEISGSSESWRAPMFWSWHSATPTNTIDPERITQIPVKAHTLQSGTITVVRGPQFTG 490	Qy	593	YINKTMNKDDDLTLYQTFDLATINNSMGSGDKNELLIGAEFSVNEKYIDKEFIPVQ 652
Qy	539	NLFLPKKESSNSIAKPKTYTNSAALLQYRVRTRIYASTNLRFLPVQNSNDLVIYINKT 598	Db	551	-FSATMSSGSNLQSGSFRLHGLFTTPFNSNGSSVFTLSAHVNSCGNEVYIDRIEFVPAEV 609
Db	491	DI - LRRTGGPFTVNNINGQPLQYRTRIYASTNLRFLPVQNSNDLVIYINKT 548	RESULT 23		
Qy	599	NKDDDLTYQTFDLATINNSMGSGDKNELLIGAEFSVNEKYIDKEFIPV 650	A41052		
Db	549	DTGDPPLTFQSFSTATINTAFTFPMQSSTTVGADTFSSGNEVYIDRFELIPV 600			
			C:Species: Bacillus thuringiensis		
			C:Date: 03-Apr-1992 #Sequence_revision 03-Apr-1992 #text_change 09-Jul-2004		
			C:Accession: A41052		
			R; Lee C.S.; Aronson, A. I.		
			J. Title: Cloning and analysis of delta-endotoxin genes from <i>Bacillus thuringiensis</i> subsp R; Lee C.S.; Aronson, A. I.		
			A:Reference number: A41052; MUID: 92011442; PMID: 1655719		
			A:Accession: A41052		
			A:Status: preliminary		
			A:Molecule type: DNA		
			A:Residues: 1-1181 <LBB>		
			A:Cross-references: UNIPROT:Q03748; GB: M65252; NID: 9142875		
			C:Superfamily: parasporal crystal protein		
			C:Keywords: delta-endotoxin		
			Query Match 26.1%; Score 888; DB 2; Length 1181;		
			Best Local Similarity 34.6%; Pred. No. 1.1e-48;		
			Matches 206; Conservative 107; Mismatches 222; Indels 60; Gaps 18;		
Qy	139838	parasporal crystal protein - <i>Bacillus thuringiensis</i>	Qy	82	VPPAGALTSPYQSPFLNTW --- -PSDADPWAKFMAQVEVLIDKKEEYAKSKALALQQL 137
C:Species: <i>Bacillus thuringiensis</i>			51	VPGAG --- -FVLGLIDLIWGFVCPSQ --- -WDAFLVQIEQLSQRIEEFARNQASRLEG 103	
C:Date: 19-Jul-1996 #Sequence_revision 19-Jul-1996 #text_change 09-Jul-2004			138	QNNFEDYNNALNWKTKPLSLRSRQRDRIFLSQASBHFRRNSMPSFAVSKFELVFLPT 197	
C:Accession: 139838			198	YAOAANTHLLIKDQVGFGEENYSEDVAEYTHRQLKLTQOYTDHCVNTWVNGLNGR 257	
R; Hefford, M. A.; Brouseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J. A.; Lau, P. C. K.			104	SNLYQIYAAEAFRWEADPTN - PALREENRIQ - -FNDMNSALTAIPPLFTVQNYQVPLLSV 160	
J. Biotechnol. 6, 307-322, 1987			161	YVQAVNLHLSVLDSVQWRNLQDVAATINSRNDRSFTAVSKFELVFLPT 197	
A:Title: Sequence of a lepidopteran toxin gene of <i>Bacillus thuringiensis</i> subsp kurstaki			220	STYDAAVVKPNRFRREMLTUVLIVLFFPYDIRLYSKGVKTELTRDIFTDPFISLNTLOE 317	
A:Reference number: I38838			221	PDSRDWVRYNQFRELTUTVLDVLSFENYDSRTYPIRTVSQLTREIVTNPV --- -LEN 275	
A:Accession: 139838			Qy		
A:Status: preliminary; translated from GB/EMBL/DBJ			Qy		
A:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Qy		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Qy		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Db		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
A:Residues: 1-1155 <RES>			Qy		
A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Db		
C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Qy		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Db		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Qy		
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A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Qy		
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C:Keywords: delta-endotoxin			Qy		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
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Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Qy		
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C:Superfamily: parasporal crystal protein			Db		
C:Keywords: delta-endotoxin			Qy		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
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Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
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C:Keywords: delta-endotoxin			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
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A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Db		
C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Db		
C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
A:Residues: 1-1155 <RES>			Qy		
A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Db		
C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
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Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Keywords: delta-endotoxin			Db		
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Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
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A:Cross-references: UNIPROT: P06578; GB: M37263; NID: 9142885; PID: 9142886			Db		
C:Superfamily: parasporal crystal protein			Qy		
C:Keywords: delta-endotoxin			Db		
Query Match 26.3%; Score 895.5; DB 2; Length 1155;			Db		
Best Local Similarity 33.3%; Pred. No. 3.3e-49;			Qy		
Matches 220; Conservative 118; Mismatches 233; Indels 91; Gaps 24;			Db		
A:Residues: 1-1155 <RES></					

Qy	431	DQKNETSTQTYDSSKRNNGHVSQADSIDQLPPTTDEPLEKAYSHQNLNYAECFLMQDRRG	490
Db	393	LTTNLPLST---IYRQRTV--	443
Db	491	I----PFFTWTHRSVDFNTIDAEKITQLPVKAYALSSGASILBGPGFQGNLFLKE	545
Qy	444	YTLRRAPISTWQHSAEFPNNIIPSSQITQPLTKSTNLGSGTSVVKPGFTCGDIL-RRT	502
Db	546	SSNSIAKFKVTLNSALLORYVRVRYAATSNLRLFVQ-----NSNNDFLVIVYINKTMN	599
Db	503	SPGQITSLRVNITAPLSSQYRVRVRYAATSNLQFHTSIDERPINOGN-----FATM	555
Qy	600	KDDDLTYQFDLATTNSNMGFSGDKNELIIGAESFSNEKLYIDKIEFPIYQL	652
Db	556	SGSNLQSGSPRTVGGTTPEFNSSGSSVFTLSAHPVNSGNENVYIDRTEFVPAEV	608
RESULT 26			
A22798		parasporal crystal protein - <i>Bacillus thuringiensis</i>	
C;Species:		Bacillus thuringiensis	
C;Date:	23-Aug-1987	#sequence_revision	09-Jul-2004
C;Accession:	A22798		
R;Shibano, Y.; Yamagura, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.			
Gene 34, 243-251, 1985			
A;Title:	Nucleotide sequence coding for the insecticidal fragment of the <i>Bacillus thuringiensis</i> protein		
A;Reference number:	A22798; MUID:85232070; PMID:2989108		
A;Accession:	A22798		
A;Molecule type:	DNA		
A;Residue:	1-934 < SHI>		
A;Cross-references:	UNIPROT:Q9SSV8; GB:M10917; PID:g143100; PID:AAA22552.1; PID:9551713		
C;Comment:	The authors translated the codon ACA for residue 264 as Ser.		
C;Superfamily:	parasporal crystal protein		
C;Keywords:	delta-endotoxin		
Query Match	25.7%	Score 874, DB 2, Length 934;	
Best Local Similarity	32.9%	Pred. No. 5.9e-48;	
Matches	215	Mismatches 240; Indels 78; Gaps 22;	
Db	31	DNPNTSLELNKYEFLRMTEDSSTEYLDNSTVKDAGTGTSVVG-----QILGVGVPF	84
Qy	3	NNPNIN-EIPIY----NCLSNPNEVFLGGERIE---TGTPIDSLSLTQFLLESEFVPG	53
Db	85	AGALTSTFYQSFLNTIW---PSDADPKAFMAQEVFLDKIEEYAKSKALAEQCLQNN	140
Qy	54	54 AG---FVGLVDLIIWGTFGPSQ---WDAFLVQTLTQFLINORIEEPARNOAISRLCGLSNL	106
Db	141	PEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAEHFRNMSMPSAVSKBEVLFPLTYAQ	200
Qy	107	YQIYAESPREWEADPTN-FALREEMRMIQ---FNDKNSALTAIPLEFAVQNYQVPLLSVYVQ	163
Db	201	AANTHLLPLKDAQVFGEEGYSSEDVAEFTYHRQLKLTOQYTDHCVNWYNGLNRGSTY	260
Db	164	AANLHSVRLDVSFQGRMGFDAATINSRNDLTRLIGNNTDYARWINTGLERWGPDS	223
Db	261	DAWVYKFNFRREMTLTVLTLIVLFFYDRLYSKGVKTELTRDITDPIFSLNTLQBYGP	320
Qy	224	RDWVYRQNFRELLTVLIVLVALFSNYDSRRYPIRTVSQLTRETYTNPV-----LENFDG	278
Db	321	TFSL---IENSTRKPHFLDYLQGIEFHTPLQPGYFGKDSFNYWGNYVETRPSGSSK	376
Qy	279	SPRGMQAQREONIROPHMLDILNRITIYDVRHG----FNYNSGHQITASPVGFSGP	332
Db	377	ITSPYFGDK-STEPVQKLSFQDGOKVYRTIAN----TDVAAWPNQKVLYGTVKVDQSVD	430
Db	333	PAPLFGNAGNAAPVPLVSLTGLGFRTLSSPLYRILGSGPNQKELPFYLDGTBPSFAS	392
Qy	431	DQKNETSTQTYDSSKRNNGHVSQADSIDQLPPTTDEPLEKAYSHQNLNYAECFLMQDRRG	490
Db	393	LTTNLPLST---IYRQRTV--	443

Db	444	VYTLRAPTSWQHRAEFNNNIPSSQTQIPLTKSTNLGSGRSVKGGFTGGDIL-RRT	502
Qy	546	SSNSTAKFKVTLNSALLQLQRVVRIRYASTNTNLRLFWQ-----NSNNDFLVYINKTMN	599
Db	503	SPQGSTLRLNNT-APLSPQRVVRIRYASTNTNLQFHTSIDGRPINQGN-----FSATMS	555
Qy	600	KDDDLTYQFDLATNSNMCPGDKNBLIAGESFVSYNEKVIDKIERIPVQL	652
Db	556	SGSNLQSGSFRTVGFTPPNFNSGSSVFTLSAHVFNNSGEVYIDRIFEVPAEV	608
RESULT 27			
Qy	JC2219	parasporal crystal protein cryAA - <i>Bacillus thuringiensis</i>	
C	Species: <i>Bacillus thuringiensis</i>		
C	Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004		
C	Accession: JC2219		
R	Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.		
B	Biotech. Biotechnol. Biochem. 58, 830-835, 1994		
A	Title: Cloning of a new cryIA (a) gene from <i>Bacillus thuringiensis</i> strain FU-2-1.		
A	Reference number: JC2219, MUID:94289859; PMID:7764972		
A	Accession: JC2219		
A	Molecule type: DNA		
A	Residues: 1-1176 <UDA>		
A	Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:9506190; PIDN:BA004468.1; P		
C	Generics:		
A	Gene: cryIA(a)		
C	Superfamily: parasporal crystal protein		
C	Keywords: delta-endotoxin		
Query Match	25.5%	Score 870; DB 2; Length 1176;	
Best Local Similarity	32.8%	Pred. No. 1.5e-47;	
Matches	214;	Mismatches 241; Indels 78; Gaps 22;	
Qy	31	DNPNSTLLEFLINYKEFLRIMPDSSTEVLDNSTVKDAVGTGIVSVG-----QIIGVGVYGP	84
Db	3	NNPNIN-ECIPIY---NCLSNPEVVLGGERIE---TGYPTBDISLSLTQFELSEFVPG	53
Qy	85	AGALTSPYQFSFLNTIW----PSDADPWAKFMAQVEVLIIDKTEYAKSKALABQLQNN	140
Db	54	AG----FVGLGLDIIWGIIFPSQ---WDAFLVQIEQINQRIBEPANOQASISLGLQSLN	106
Qy	141	FADFLVNLNSWKLPSLRLRSKRSQDRIFELPSQAEHSFRNSNMPSPFAVSKFEVLFPLPTYAQ	200
Db	107	YQIYAESPREWEADPTN-PALREEMRIQ----FNDMNSALTTAIPLLAQNYQVPLLSVSVQ	163
Qy	201	AANTHLLIJKDAQVEGENYSSSEDAEYTHRLQLKLTQYDHCUNMYVNGLNLRGSTY	260
Db	164	AANLHLSTVIRDVSFGQRGFDAAINSRNDLTRLIGNTYDAVRYNTGHLERWVGPD5	223
Qy	261	DAWYKPNPRPREMTLVLDLIVLPPDYIRLYSKGVTELRLDIFTPIFSNLTLQEQYGP	320
Db	224	RDNWRYNQQRRELTIVLTVLDLVALFNSYDSRSPYRPTVSQLTREIYNPV-----LENPDG	278
Qy	321	TFLS----IENSTRKPHLFDYLOGIEBFHTRLQPGYFGKDSFNYWGSNQYVETRPSIGSSKT	376
Db	279	SFRMAMQRIBONRQPHMDILNSITYDQHVRG-----FNYWGSQGQITASPVGFSPB	332
Qy	377	ITSPRYGDK-STEPVQKLSPEDGQKRYPTIAN----TDVAAWPNGKRYLGLVTKVDFSYQD	430
Db	333	FAFPFLGNGNAAPEPVLSLTLGLGFRTLSSPLYRRLTILGSGPNNQELFLVLDGTEFSPAS	392
Qy	431	DQKNETSTOTYDSKRNNGHIVSAQD51DQLPBPETDDEPLKAYSHQUNYAECPLMQDQRGT	490
Db	393	LTTNLPST---IYRQRTV---DSDLVIFPQDNSSPPRAGFSHR1SHV--MLSQAGA	443
Qy	491	I-----PFFTWTHRSVDFNTIDAKITOLPVVKAYALSSGASIIIEGPGFTGQNLFLFLKE	545
Db	444	VYTLRAPTSWQHRAEFNNNIPSSQITPLTKSTNLGSRTSVKPGFTGGDIL-RRT	502
Qy	546	SSNSIAKFKTINSLALLQYRVRIRYASFTNLRLFVQ-----NSNNDFLVYINKTMN	599

RESULT 31
DSBXSH crystal protein cry1Ac1 [validated] - *Bacillus thuringiensis* subsp. *kurstaki*
Species: *Bacillus thuringiensis* subsp. *kurstaki*
Date: 18-Apr-1994 #sequence_change 09-Jul-2004
Accession: A23962 #text_change 31-Dec-1992
Title: Characterized full-length and truncated plasmid clones of the crystal protein cry1Ac1

RESULT 32
S32645
parasporal
C; Species:
C; Date: 20

crystal protein cry1Gai - *Bacillus thuringiensis*
Bacillus thuringiensis
-Feb-1995 #sequence revision 20-Feb-1995 #text change 09-Jul-2004

C;Accession: S32645
 R;Lambert, B.
 Submitted to the EMBL Data Library, April 1993

A;Reference number: S32645
 A;Accession: S32645
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1166 <LAM>
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

A;Residues: 1-1176 <SCII>
 A;Cross-references: UNIPROT:P02965; GB:MI1250; NID:9142764; PIDN:AAA22353.1; PID:9142765
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match	25.4%	Score 866;	DB 2;	Length 1176;
Best Local Similarity	32.8%	Pred. No. 2.7e-47;		
Matches 214;	Conservative 119;	Mismatches 242;	Indels 78;	Gaps 22;
Qy	31 DNPNSTLLELNKEFLRMTEDSSTEVLNDSTVKDAVGTGTSVVG --- QIGVGVVF 84			
Db	3 NNPNN-ECIPY --- NCLSNPEVEVLGGERIE --- TGYTPIDISLSTQFLLSEFVPG 53			
Qy	85 AGALTTSFYQSFNLNTW --- PSDADPKAFLMAQEVLIDKKEVAKSKALAELOGLNN 140			
Db	54 AG --- FVGLVDIWIWIGIFGPQS --- WDAFPVQEQLINORIEFARNQAIISRLLEGLSNL 106			
Qy	141 FEDVYNALNSWKTKPLSLRSKRSQDRIRELFSQAEHSFRNSMPSFAVSKEVLFLPFTYAQ 200			
Db	107 YQIAYASFREWEADPTN-PALREENRQ --- FNDMSNLTAIPLAVQNYQVPLISVYVQ 163			
Qy	201 AANTHILLKKDAQVPGEEGYSSEDVAEFTHRQLKLTQYTDHCVNWNNGLNGRGSTY 260			
Db	164 AANLHLISVLURDVSPVFGQRNGFDDAINTNSRNLDTLIGNTDYAVRNWTGLERWGPDS 223			
Qy	261 DAWKVKRNFRERMLTIVLDLVLPPFYDRLYSKVKVLTTRDFTDPIFSLNTLQEYGP 320			
Db	224 RDWVRYXNQFRRELTLTVDIVALEFNYDSRRYPIRTVSQITRELYTNPV --- LENFDG 278			
Qy	321 TFLS --- TENSIRKPHLFDYLOGIEFHTRLQPGYFGKDSFNTYNGGNYVTRPSIGSSKT 376			
Db	279 SFRGMAQRIEQNIROHMDILNSLTTIYTVDVHRG --- FNTYNSGHQITASPVCFSGPE 332			
Qy	377 ITSPFYGDK-STEPVQKLSPDGOKVYRTIAN --- TDV/AWPNCKVYLVGTVKDVSQYD 430			
Db	333 FAFLPLFGNAGNAAPPLVLSUTGLGFRITPSLYPRRLQGSPNQELFWLGDTSFSFAS 392			
Qy	431 DQKNETSTQYDSKRNNGHVSAQDSTDQLSPETTDDEPLEKAYSHOLNYACFLMDRRGT 490			
Db	393 LTINNUFST --- IYQRGRTV --- DSDDVTPQDNEVPPRAGFSHRLSHVT - MLIQQAAGA 443			
Qy	491 I --- PFFTWTWHSYDFFFNTIDAERITQLOPFPVRAYALSGASTIEGPFTGNLILFLKE 545			
Db	444 VYTLR2APTSWQHRSAAEENNIIIPSSQITQPLTKSTNLGSGTSVVKGPGFTGGDIL - RRT 502			
Qy	546 SSNS1PAKEVTLNSAALLQRYTRVYRTRAYASTNLRLFVQ --- NSNDPLIVYIYNTKNN 599			
Db	503 SPQQTSTLRYN-TAFLSQRTRVYRTRAYASTNLQPHTSIDGRPQNQN --- FSATMS 555			
Qy	600 KDDDLTYQTPLATINNMGSFGDKNELIGAEFSVNEK1Y1DKEFIPVOL 652			
Db	556 SGSNLQSGSFSRPTVGFPTPNFSNGSSVFTLSAHVNSGNVEVYDIEFVPAEV 608			
RESULT 34				
S02215	parasporal crystal protein cryA - <i>Bacillus thuringiensis</i> (strain entomocidus)			
C;Species: <i>Bacillus thuringiensis</i>	C;Sequence: #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004			
A;Title: Nucleotide sequence of a gene cloned from <i>Bacillus thuringiensis</i>				
R;Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.				
Nucleic Acids Res. 17, 446, 1989				
A;Reference number: S02215; PMID:8908405				
A;Accession: S02215				
A;Status: translation not shown				
A;Molecule type: DNA				
C;Accession: A22617				
R;Schnepp, H.E.; Wong, H.C.; Whitley, H.R.				
J. Biol. Chem. 260, 6264-6272, 1985				
A;Title: The amino acid sequence of a crystal protein from <i>Bacillus thuringiensis</i> deduced				
A;Reference number: A22617; PMID:85207613				
A;Accession: A22617				
A;Molecule type: DNA				
Query Match	25.4%	Score 866;	DB 2;	Length 1176;

Qy	202	ANTHILIKDAQVFGREWQISSVEDAEIFYHQLKLTQQTIDCYNWYNGLNGRSTYD	261	Db	259	ATQLTREVYDLPINENLSPAAASY-PTFSAEASAIIRSPHLVDFLNSFTIYT-----	310		
Db	163	ANLHSLRDAVSGGWDLQDIAVNNHYNLINLHRYEHCLDYNQLENIGTNTR	222	Qy	353	GDGS--FNYWSGRVYERPSISSLSSKTTTSPFVG-DKST-EVQKLSPDQKRYTANT	407		
Qy	262	AWKVKENFRERMTLTVLDLIVLFPFDYIRLYSKGVKTELDRDIFTDPIESLNTLQEXGPT	321	Db	311	-DSLARYAYWGGHLVNSFRGTTTINLRLSPLYGRECNERPTITASPSVP1FRTLSY-	367		
Db	223	QWSRNFQRFRELTIVLDLIVLFPNDARAVPICTSSVSDPSVANIPN	282	Qy	408	DVAAPWNGKVKVDFQSYODQNETSTQYDSKRNGHVAQDSIDOLQPETDTP	467		
Qy	322	-FLSTIENSIKRPHFLDFLQGIEFT---RIQPGFQGDSNFYNGNVTETRPSIGSSKTT	376	Db	368	-ITGLDLSNPVAGIEGVF-----QNTSRSY--RKGSP1--DFSESELPPQDASYS	414		
Db	283	GENRAEGFVRPFPHMDEMNSL-FVIAETVRSQ-----TVWGGHLVSSRNTAGN-P	330	Qy	468	LEKAYSHOLNYAECFLMQDR---RGTIPEFTWTHSYDFENTIDAEKTFQTLPVVKAYAL	523		
Qy	377	ITSPFYG-----DKSTEPVQKLSPDFQKQYKRTIANTDV-AAMWNGKVKYLGVTK	423	Db	415	PAIGYSHRLCHA-TFLERISGPRIAGTV-FSMWTHRSASPTNEVSPSRTQIPWVKAHTL	471		
Db	331	INFPYIGIFNPGGAIWADPDRP-----FRTLSDPFPVTRGGPFPNHYTUGRG	380	Qy	524	SSGASITIEPGFGFTGNNLFLIKESSNSIAKFKVTLNSAQLQRVRIYASTNMRLFVQ	583		
Qy	424	VDFSQDDQKNETSTQTYDSKRKNNGHVSQAQDSIDOLQPETDPELEKAYSHOLNYAECF	482	Db	472	ASGSVIKGKFGFTGQDIL-TRNSMGEGLTRVTS-TGRLPQSXYTRFASVANRSGTR	529		
Db	381	VAFOQ-----TGTNHTRTRFNSGTT-----DSLDEPAPONGSAPWNDYSHVLAHNTVFR	430	Qy	584	NSNNDFFLPYINKTMKDDDLTYQTFDIAATTNSNNGFSDDKNELLGAESFVSNEKIVYD	643		
Qy	483	-----LMQDRGTTIPFPTWTHSYDFENTIDAEKTFQTLPVVKAYALSSGASLIEGQFTG	538	Db	530	YSQPPSYG1SFPKTMDAEGLPLTSRSFAHTTLEPFTPTFSRAQEEDFLYIQS-----GVIYD	584		
Db	431	WGEIAGSDSRAPMFSTWTHRSADRTNINNPNTITQLPATAHNLHSGSTVVRGPQFTG	490	Qy	644	KIEFIPV	650		
Qy	539	NILFLKKESSNSTIAKFKVTLNSAALLORYVRVRLYASTTNLFLFVQNSNNDELVIVINKTM	598	Db	585	RIEFIPV	591		
Db	491	DLI-RRPNTGFTADIRYNT-TCPLSQQYRVRVRYASTDLOFFTRGTSUNQGNFQTM	548	RESULT 38					
Qy	599	NKDDDLTYQTFLATINNSMGFSGDKNELLIGAESPVSNEKIVYDKEFIPVQL	652	S32647					
Db	549	NRGNLNESGNFRNTAGFSTPFSFSNAQSTPFLGTQAF-SNQEVYIDRIEFVPAEV	601	parasporal crystal protein cry1Dbl - Bacillus thuringiensis					
C:Database: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004									
C:Accession: S32647									
R; Lambert, B.									
submitted to the EMBL Data Library, April 1993									
A;Species: Bacillus thuringiensis									
A;Reference number: S32645									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1160 <LAM>									
A;Cross-references: UNIPROT:045747; EMBL:222511; PIDN:9295863; PIDN:CAA80234.1; PID:9295864									
C:Sequence: Bacillus thuringiensis									
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
R; Hoeft, H.; Soetaert, P.; Jansens, S.; Peferoen, M.									
Nucleic Acids Res. 18, 5545, 1990									
A;Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific parasporal crystal protein									
C:Keywords: delta-endotoxin									
C:Accession: S11446									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1165 <HOB>									
A;Cross-references: UNIPROT:P19415; EMBL:X54160; PIDN:940279; PIDN:CAA18099.1; PID:940280									
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C:Database: 21-Jun-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
S11446									
parasporal crystal protein cry1D - Bacillus thuringiensis									
N;Alternate names: parasporal crystal protein cry1D									
C:Species: Bacillus thuringiensis									
C:Accession: S11446									
R; Lambert, B.									
submitted to the EMBL Data Library, April 1993									
A;Reference number: S32645									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1160 <LAM>									
A;Cross-references: UNIPROT:045747; EMBL:222511; PIDN:9295863; PIDN:CAA80234.1; PID:9295864									
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C:Database: 21-Jun-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
S11446									
parasporal crystal protein cry1D - Bacillus thuringiensis									
N;Alternate names: parasporal crystal protein cry1D									
C:Species: Bacillus thuringiensis									
C:Accession: S11446									
R; Lambert, B.									
submitted to the EMBL Data Library, April 1993									
A;Reference number: S32645									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1160 <LAM>									
A;Cross-references: UNIPROT:045747; EMBL:222511; PIDN:9295863; PIDN:CAA80234.1; PID:9295864									
C:Sequence: Bacillus thuringiensis									
C:Database: 21-Jun-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
S11446									
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N;Alternate names: parasporal crystal protein cry1D									
C:Species: Bacillus thuringiensis									
C:Accession: S11446									
R; Lambert, B.									
submitted to the EMBL Data Library, April 1993									
A;Reference number: S32645									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1160 <LAM>									
A;Cross-references: UNIPROT:045747; EMBL:222511; PIDN:9295863; PIDN:CAA80234.1; PID:9295864									
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C:Database: 21-Jun-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
S11446									
parasporal crystal protein cry1D - Bacillus thuringiensis									
N;Alternate names: parasporal crystal protein cry1D									
C:Species: Bacillus thuringiensis									
C:Accession: S11446									
R; Lambert, B.									
submitted to the EMBL Data Library, April 1993									
A;Reference number: S32645									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-1160 <LAM>									
A;Cross-references: UNIPROT:045747; EMBL:222511; PIDN:9295863; PIDN:CAA80234.1; PID:9295864									
C:Sequence: Bacillus thuringiensis									
C:Database: 21-Jun-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C:Accession: S11446									
S11446									
parasporal crystal protein cry1D - Bacillus thuringiensis									
N;Alternate names: parasporal crystal protein cry1D									
C:Species: Bacillus thuringiensis									
C:Accession: S11446									
R; Lambert, B.									

Qy	363	NYVETRPSGSSKTTISPFNG-DKSTE-PVQKLSFDGQKYRTIA-----NTDVAAWP	413
Db	322	HLVNSFRGTTGTTNLIRSPLYREGCTERTPTTISASPSVFRTLSYFTGLNNNNPVA--	378
Qy	414	NGKVYGLTKVDFSCYDDOKNETSTQTYD5KRNNGHVSQAQSIDOLPPETDEPLBKAYS	473
Db	379	-----GIEGVFP-----QNTISIY--RKGSDP-----DSFSBPPQDVSVPAIGYS	420
Qy	474	HQLYNAAECFLMQR---RGTIIPFTWHRSDFFNTIDAEEKITOLPVVKAYALSSGASI	529
Db	421	HRLCHA-TFLERISGPRIACTV--FSWHRSSASPNEVSPSRITQPVWKAHTLWASGV	477
Qy	530	IEGPFTGCGNLFLFEKESNSIAKFKYTLNSAALLORYVRIRYASTNLRLFVQNSNNDF	589
Db	478	IKGPFGTGSDIL-TRNSMGDLGALRVTP-TGRLPQSYVYERVASVANRSGTFRSQPPS	535
Qy	590	LVYIINKTMKNDQDLYTQFDLATTNSNMGFSGDKNEELIGAESFVSNEK1YIDKIEFIP	649
Db	536	YGIISPXPKTMAGEALTSRSFAHTTLPITFSRAOBEDFLYIQS-----GVYIDRIBFIP	590
Qy	650	V	650
Db	591	V	591
RESULT 39			
Qy	A29838	parabporal crystal protein - <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i>	
C;Species	Bacillus thuringiensis subsp. kurstaki		
C;Date	08-Mar-1999		
C;Accession	A29838	#Sequence_revision 08-Mar-1999 #text_change 09-Jul-2004	
R;Thorne, L.; Garduno, F.; Decker, D.; Zounes, M.; Wild, M.; Walfeld, A.M.J.; Bacterio, I. 166, 801-811, 1986			
A;Title	structural similarity between the Lepidoptera- and Diptera-specific insecticida		
A;Reference number	A94672; MUID:86223796; PMID:3011746		
A;Accession	A29838		
A;Molecule type	DNA		
A;Residues	1-1156 <THO>		
A;Cross-references	UNIPROT: P06578; GB: M12661; PID:g143226; PID:AAA22613.1; PID:g143227		
C;Superfamily	parasporal crystal protein		
C;Keywords	delta-endotoxin		
Query Match	23.8%	Score 809; DB 2; Length 1156;	
Best Local Similarity	31.9%	Pred. No. 1.2e-43;	
Matches	212;	Conservative 116; Missmatches 238; Indels 98; Gaps 26;	
Qy	31	DNPNSTLLEFLNYKEFLRMTEDSSTEVLNDNSTVKAAGVGTG1SVVG-----QILGVGVPF	84
Db	3	NNNNPNE-ECIY ---NCLSNPEYVGLSERIE---TGYPIDISLSLTQFLISBFVPG	53
Qy	85	AGRLTSPYQOSFLNTW---PSDADPKAFMAQVEVLIDKKEETAKSKALAELOGLQNN	140
Db	54	AG---FVIGLVDIIGFIFGPSQ---WDAFLVQIEQLINORIEEFARNQANISRLGQLSNL	106
Qy	141	FEDVNAIANSWKEPLSLRSKRSQDIRELFSQAEHFRNMSPFAVKPEVLFPTYAQ	200
Db	107	YQYAAESPREWEADPTN-PALREEMRIQ--FNDMSALTAITPLAVQNYQVPLISVYQ	163
Qy	201	AANTHLLLKKDAQVGEENGQSSSEDAEFPYTHROLKLTQXYTDHCHCNWYNGLNGLRGSTY	260
Db	164	AANLHLSVLRDVSFGQWGFDAATINSYNDLTLIGNYTDHRTWYNTGLERWGPDS	223
Qy	261	DAWKFKNFERNRMLTVDLIVLPYDRLYSSVKTELTRDIEFTDPLFSLNTQOEYQG	320
Db	224	RDWIRYQNRERELTIVLDDIVSLFPNYDSRTYPIRTVSQITREYTNPV---LENFDG	278
Qy	321	TF ---LSTENSIRKPHLFDYQSTEFHTRLQPGYFGKDSFNYMSGNYVETRPSIGSSKT	376
Db	279	SFRGSAQGIEGSIRSPLMDILNSTIYDAHRGYI-----YNGHQ1MASPVGSGPE	332
Qy	377	ITSPPYGDK---STEPVQKLSFSD---GQKYRTIANTDAAWNGKVY---LGVTKDFSQY	429
Db	333	FTEPLXGTMGNNAAPQORTIAVOLGQSYVRLST-----LYVRPENGTNNNOQISGP	383

Oy	430	DDQK-----NETSTQTYDSKRNNGHVSAQDSIDOLPPETTDEPIEKAYSHQ-LNYAECF	482
Db	384	DGRICWNLKEGQPPTEK-----ABVDSPPBIPQNNAVPQRQFSHRCLAYVSMF	438
Oy	483	IMQDRRTGTPFF-----TWRHRSVDFENTIDABKITQLPVRKAYALISSA-SIIEGPG	534
Db	439	YSGFSNSSSSVIRAPNDSWTCGAAEFDVIPSQQTQLPLTK---LQSQMLWNNSVYKGLG	495
Oy	535	FGGNLILFLKESSNSIAKEPKVTLNSSAQLQYRTRIYASTTNURLFVQ-----NSNNND	588
Db	496	PTQGDI---LEBLTQISLVRVNL-TAPLSQRYRTRIYASTTNQFHTS1DGRPAQGN-	551
Oy	589	FLVIVYINKTMNKKDDLTYQTFDLATTNSMGFSGDKNELLIGAESFSVNEKIV1DKIEFI	648
Db	552	-----FSATMSSGSNLQGSFRTVGFTTPBNFSNGSSVFTLSAHVNSGNEVY1DRIEFV	606
Oy	649	PVQJ	652
Db	607	PAREV	610
RESULT 40			
	532689	Parapsoral crystal protein cry1Hal - <i>Bacillus thuringiensis</i>	
Oy		C;Species: <i>Bacillus thuringiensis</i>	
Db		C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004	
Oy		C;Accession: S32689	
Db		R;Lambert, B.	
Oy		Submitted to the EMBL Data Library, April 1993	
Db		P;Reference number: S32645	
Oy		P;Accession: S32689	
Db		P;Status: Preliminary	
Oy		P;Molecule type: DNA	
Db		P;Residues: 1-1172 <1AM>	
Oy		P;Cross-references: UNIPROT:Q45748; EMBL:722513; NID:9296086; PIDN:CAA80236_1; P	
Db		C;Superfamily: parapsoral crystal protein	
Oy		C;Keywords: delta-endotoxin	
Query Match			
Best Local Similarity			
Matches	203;	Score 787.5; DB 2; Length 1172;	
	Conservative	Pred. No. 2.8e-42;	
		MisMatches 243; Indels 91; Gaps 21;	
Oy	19	ELQTNHQQ---YPLADNPNS---TLEBLNKEFLRMTEDS-STEVLNDNSTVKDAVGRTGI	70
Db	2	ELINNQQYQVNCNSLSPENEIDLSSRSRREQAETSLGLTRFLLESLLPFGA-SFGF	60
Oy	71	SVVGQIIGVGVGPAGALTSFQSLNLTWPSADPWFKAQVPEVLIDKIEETAKSA	130
Db	61	ALFDIIGVIG-----PDQWNLFLAQEQLIDQRIEAVHRNQA	98
Oy	131	LAELOGLQNNFEDYVNAALNSWKKTPLSLRSRSRQDRRELFSQAEQSHFRNSMPSFAVSKF	190
Db	99	ISRLLEGIGDSDYEVYIISLREWEASP--NNEALQDQVNRFSNTNDALITAIP1LREQGF	155
Oy	191	EVLPLPPTQAOANTHLLIKLDAQVEGEGYSSVEDAAYFYHQLKLTTQOYTDHCYWNWNV	250
Db	156	EIPLLSTYVQAOANLHLSSLRDAVYFGQRWGLDVTYVNNHNLINITYSDHCAQWENR	215
Oy	251	GGNGLSTERDWAVKPFRFRRTTLYLIVLFFPLRYSKGKVTDLTRDIFTDPI-	309
Db	216	GIDNFGGVs---ARYLDFORETTISLIVDIAFLPNIDRTYPTISTQSOLTRTEYTSPVA	271
Oy	310	---FSLNLQQEYGPFTLSTIENSIRKPHLFDYLOGIEFHTRLQPGYFKDSEFNWMSGNYVE	366
Db	272	EPGASLNA-----NLQNLTREPFLTRLVTGQVQSYI-----RVAHEIS	316
Oy	367	TRPSIGSKITTSPPYGDKSTPQVKQESFD---GQVYRTIA---NTDVAAPN-GK	416
Db	317	SRTTGNLSSNIQFPLG---TAASADRAFNMTTHSETTYRLSAPITYVSVSGG1SPNRTR	373
Oy	417	VYGVTRVDFSDQYDDQNEKSTOYDSRNNGHVSAQDSIDQLPETTDPLEGAYSHQ	476

374 VVEGVR--FLLIARDNNLDLPLFLY--RKEGTL--DSFTELPPEDESTPPYIGYSHRL 424
 Db 374 VVEGVR--FLLIARDNNLDLPLFLY--RKEGTL--DSFTELPPEDESTPPYIGYSHRL 424
 Qy 477 NYAE----CFLMODRRTGPFFTWTHTSRSTDFENTIDAECKITQPLPVKAYALSSGASIE 531
 A;Title: Nucleotide sequence of a novel delta-endotoxin gene cryIG of *Bacillus thuringier*
 A;Reference number: S19306; MUID:92070568; PMID:1660003
 A;Accession: S19306
 A;Cross-references: UNIPROT:Q99031; EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:g40271
 A;Molecule type: DNA
 A;Residues: 1-1156 <SM0>
 A;Cross-references: UNIPROT:Q99031; EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:g40271
 A;Experimental source: subsp. *Galleriae*
 A;Experimental source: subsp. *Galleriae*
 A;Accession: S23588
 A;Molecule type: protein
 A;Residues: 24-34 <SM0>
 A;Experimental source: subsp. *Galleriae*
 A;Experimental source: subsp. *Galleriae*
 A;Cross-references: EMBL:X58534; PIDN:CAA41425.1; PID:9488880
 A;Cross-references: PIDN:CAA41425.1; PID:9488880
 C;Accession: B42459
 R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
 J. Bacteriol. 173, 3966-3976, 1991
 A;Title: Isolation and characterization of a novel insecticidal crystal protein gene from *Bacillus thuringiensis* subsp. *kurstaki* - a little identification of an insecticidal crystal protein from *Bacillus thuringiensis* D5
 A;Reference number: A44847; MUID:92211329; PMID:1565566
 A;Accession: A44847
 A;Status: preliminary
 A;Molecule type: DNA
 C;Species: *Bacillus thuringiensis* (strain aizawai) (frag
 C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
 C;Accession: B42459
 R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
 J. Bacteriol. 173, 3966-3976, 1991
 A;Title: Isolation and characterization of a novel insecticidal crystal protein gene from *Bacillus thuringiensis* subsp. *kurstaki* - a little identification of an insecticidal crystal protein from *Bacillus thuringiensis* D5
 A;Reference number: A44849; MUID:91286178; PMID:2061280
 A;Accession: B42459
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-380 <CH>
 A;Cross-references: UNIPROT:Q8KX61; UNIPROT:Q45740; GB:M63897
 C;Superfamily: parasporal crystal protein
 Query Match 20.6%; Score 700; DB 2; Length 380;
 Best Local Similarity 36.6%; Pred. No. 2..2e-31;
 Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
 Query Match 20.6%; Score 700; DB 2; Length 380;
 Best Local Similarity 36.6%; Pred. No. 2..2e-31;
 Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
 Db 1 MNPNRNRSEHTDI -----KVTPNSELQTHNHQYPLADNPNSTLEELNYKEFLRMTEDSS 53
 Db 1 MKLNPDPDKRQSPSNKAKDST-----LKNETDQLNINHEOCUKLSEYEN 50
 Qy 54 TE-VLDNSTKVDAGTGISVCGVQFLGVGVPPAGATSFYQSFNLNTWPSADPWKAEMA 112
 Db 51 VEPPVSASTIQ---TGSIAKGKLTGIVPQAVQSLYSYFILGEWLPKGKKNOWEIM 106
 Qy 113 QVEFLIDKIEEYAKSKKALAEQGLQNNFEDYNNANWSKKTPLSRSRSKSDRIRELFS 172
 Db 107 HVEELINQKISTYARNKALTDKLQGLDAIAVTHESLWVG--NRKNTTRANSVVKQYI 163
 Qy 173 QAESHFRRNMRNPSEAVSKFELVFLPTYAQANTHILLKDAQVGEENGYSSEDVAEYHR 232
 Db 164 AELMPVQKLPSFASVGEVPLIPIYQDANHILLRDAISFGKVKLSSBISTYNR 223
 Qy 233 QKLJLQOYTDHCYVWYNGVSLNGRSTYDAWKENREREMTFLTDLIIVLPPFYDRLY 292
 Db 224 QVERAGDYSHCVWYKSTGMLNLRGNTNAWSWRYNQFKDMLVLDLVALPSYDLYV 283
 Qy 293 SKGKVKTELRDIDTPISLNTLQY-----GPTFLSIENS-IRKPHLFDYLOGI 342
 Db 284 PIKTRSQLTREVYDIAIGVHPNASFASTWYNNNAPSTIESAVVMPHLDFLEQV 343
 Qy 343 FHTRLQPGYFGKDSFNNWGNMGNVETRPSIGSSKTIT 378
 Db 344 IYSLIS-RWSNTQYNNMWRGGHRLERTIGMMLNT 378
 Qy 405 IFR---VDSQACNLNDTTGCVNRAVF--YHDASRSQSRSVSYEGYRTTGTIDNPVQVNIN 458
 Db 405 IFR---VDSQACNLNDTTGCVNRAVF--YHDASRSQSRSVSYEGYRTTGTIDNPVQVNIN 458
 Qy 457 DQFPPETTDEPKAYSHQLNAYABC-----LMQDRRTGTPFTWTHSYDFENTIDAE 510
 Db 459 TYLPGENSDIPTPDTFLSTINTGGLRQVASNRSSLAVMGMTHKSLARNTINPD 518
 Qy 511 KITDLPVYKAYALSSGASIEBGPFTGQNLJFLKEESENSLAKFKVTLNSALLQRVRVRI 570
 S19306 parasprial crystal protein cry9Aa1 - *Bacillus thuringiensis*
 N;Alternative names: delta-endotoxin; insecticidal crystal protein; parasprial crystal protein
 C;Species: *Bacillus thuringiensis*
 C;Date: 01-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
 C;Accession: S19306; S23588; A44847; S14602; S14337
 R;Smulevitch, S.V.; Osterman, A.L.; Shavellev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrd

Db	577	RYASITNIRLSV--NGSFETISONLPLSTMRLGEDLRYSGFAIRENTSIRTPASPDQIR	633		Db	587	PSSTRQENATDITYADEFGYTPEPRTVNKTPEGDITLMTLYGTPNHSYN--IYTDKI	644
Qy	629	IGAESFVSNKEKIIDKIEFIPV	650		Qy	646	EFIPV	650
Db	634	LTIIEPSFIQEVYDRIEIPV	655		Db	645	EFIPI	649
RESULT 43								
B29838	parasporal crystal protein - <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> (fragment)							
C;Species:	<i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>							
C;Date:	08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004							
Db	829838							
R;Thorne, L.; Garduno, P.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.; Bacteriol, 166, 801-811, 1986								
A;Title: Structural similarity between Lepidoptera- and Diptera-specific insecticida								
A;Reference number: A94672; MUID:86223796; PMID:3011746								
A;Accession: B29838								
A;Molecule type: DNA								
A;Residues: 1-934 <THO>								
C;SuperFamily: parasporal crystal protein								
Qy	Query Match 19.5% Score 665.5 DB 2; Length 934; Best Local Similarity 28.0% Pred. No. 1.3e-34; Matches 240; Conservative 118; Mismatches 246; Indels 151; Gaps 34;							
Db	1	MNP-NNRSHBDTIKTPNS-ELQTNHNNQPLADNPNSTLIEELNAYKEFLRMDT-----51						
Qy	52	-----SSTEYLDNSTVKDAVGTG1SUVGQQLGVVYGVPPFAGALTFSYQOSFLNTIWPSDADPW 107						
Db	61	AGNPASETI-----VGYSAGI-LVVGTMGAFAPVLAAGIISPGTLPIFM-QGSPIA 113						
Qy	108	KAFKAQVEY-----LIDKIEEYAKSXAALQELQNNFEDYNALNSWKTPLSLRSK 161						
Db	114	NWQDQNLNGGRRPQEBIDKNIINVLT-----IVTPRKNQDQEFFKWEPA---RTW 165						
Qy	162	RSQDRIREFSQAE-----SHFRNSMSFAYSFKFVFLPFTAQAAANTHLLKDKAQV 214						
Db	166	ANAKAVHDIFLTLEPLIIDQDMLKNN-----ASYRIFTLPAYAQATWHNLNLKHAAT 219						
Qy	215	FGEEW-----GYSSEDIAEYHQLK-LTQQYTDHCVNWWYNGLNGLRGSTYDAMYKFN 267						
Db	220	YNNIWLQNGINPSTENNSNYQGYLKRKIQETDYCQTYNAGLTMIRTNTNATWNNY 279						
Qy	268	RFERREMILTVLDLIVLFPYDYLRYSKGKFTLTDITDPLFSLNTLQEQYGPTELSIEN 327						
Db	280	TYRLBMLTVLDLIAFPYDPEKPGVSELREYV-----NVNSDTPRTITELN 333						
Qy	328	SI-RKPHLFDYLGQIEFHTR----LQPFYFGKDFSNY-----WS--- 361						
Db	334	GLTRNPNTFTWINGGRFTRNSRBDILP---YDIFSTGNQMAFTHNTDDRNITWGAHV 389						
Qy	362	GNVYETRPIRPIGSKITTSFYGDKSTPEVKQDQKVRTRIANTDAWPNGKVKYLG 421						
Db	390	GNII-----SQTDSKVF--PYRNMK--PDKVEIVRREYSDI-----IV-- 425						
Qy	422	TKYDPSQYDQKNETSTQYDS--KRANGHVSQAQSDIDQLPPTTDEPLERAYSHOLNYA 479						
Db	426	EMIFFNSNSSEVFRYSSNSTIENNYKRTDSYM-----IPKQTKW--NNEEYHTLSY 474						
Qy	480	EC-----FLMQDRRGTTIPPTWTHRSDFDENTIDAEEKTQLPVVKAYALSSGASIIFGP 534						
Db	475	KTDNYIIFSYVRRERRVA-FSWHTTSDFDNTIDLDNTQTHALKALKVSSDKIVKPG 532						
Qy	535	FTGGNLLFLFKESSNSIAKFKVTLNSAALLQYVRIRVASTINLRLVQNSNNDFLVY 594						
Db	533	HTGCDLVIKDSMDFRVRELKNSV---RQYQVIRYIA-TNAPKTTVFLGIDTISVEL 586						
Qy	595	NKTMNKDD---DLTYQFFDLAT--TNSMGFSGDKNEL--LIGAESFSNEKEYIDKI 645						

RESULT 47

Qy 1 MNP-NRISHDHTIKVTPNS-ELQTNHQVPLADNPNSTLDEELNYKEFLRMTEDSSTEYLD 58
Db 1 MNPQNKNEYETLNASQKLNISNYTRYPIENSPKQLIQSTNYKDWLIMCQONQYGGD 60

Qy 59 NSTYKDA--VGTG1SUVGQIQLGVG--VPGAGALTFSYCFSLNTIWP--DADPKWAFMA 112
Db 61 PETFDGGELASVTTVGTVLGEGFTTFLGLALIGF-GTLIPVLFPAQDQSNTWSDFT 119

Qy 113 QVEVLIDKKEEYAKSKAKAELQCLQNNFEDYNAALNSWKKTPSLSKRSQRDIRELFS 172
Db 120 QTKNIKKEASTYISANKILNRSFNTVSTYHNHLKTWNPF--NPQNTQD-VRTQIQ 175

Qy 173 QAESHPFRNSMPSFAV--KPEVFLPLTYAQANANTHLLLKDQAVF----GB 217
Db 176 LVIYHFQNTVPELVNSCPNPSDCDYNVNLVLSYYAQANLNLHTVLNQAVKPEAYLNKR 235

Qy 218 EWGYS--EDVAEYFHQLKLTKQQYTDHCVNWNVGLNGLRSGYDA-----WVKFNR 268
Db 236 QFDYPLEPLTAIDYVPLVLTKAIDTYCIVTCYTKKGNLNIK-TIPDSNLGDNINWNTNT 294

Qy 269 FRRERMTLTVLDLTVLFPPFDIYLRSKGKVTELTRDIFTDPIFSLNTLQBYGPTFLSNTS 328
Db 295 YRTKMTTATLWVLFVLPNDVKGKPIGIVFESPYKX--DFQYQEDS 352

Qy 329 I-RKPHLFVYLOGIEFHTRLQ--PGYFGKDSFNYWSGNYVETRPSIGSSKTTSPFVGDK 385
Db 353 LTRRPHLFTWLDLSNFYERQATTPN-----NFFTSHYNNMFTYTLDNISQSSSVFENHN 405

Qy 386 STEPVQKLSFDGOKVYRTANTDVAAPNGKV--YLGYTVKDF-----426
Db 406 VTDKLKSLGL-ATNIVYIFLN--VISLDNKLNDYNNNISKMDFFITNGTRLLEKELTAGS 462

Qy 427 --SOYDDQKNETSTQYDSKRNGHVSQAQSDISDOLPPETDPELEYASHQHONYAECLM 484
Db 453 GQTYDVNRKNIQFGPLKRENOGQNPFLPTVY-----YSHLUSFIKSLI 509

Qy 485 QDRRGIT-IFPFTWTHRSVDFNTIDAETKTOLPVKAYALSSGASIEGPGFTGGNLLPL 543
Db 510 PATYKQTYVTFANTHSSVDPKNTIYTHTQFQAVKANSLGTAASKVYQGPHTGGDUDF 569

Qy 544 KESSNSIAFPKVTLNSAALQLQRVRIYAS--TTNTRLFLVQNSNNDF--LYTYINKTMM 599
Db 570 KD-----HFKITCQHSNQQSFYIRYASNSANTAVINLISIPGVAELGMALNPTFS 623

Qy 600 KDD--DLTYQTDFLATTNSNMGFQGDKN-ELIIGAEESTVSNEKUYDKEFLPV 650
Db 624 GTDVTNLKTFQYLFESNEVKFAPNQNTSLVNRSDVTTVLIDKIEFLPI 677

RESULT 48

Qy 1033 mosquitoicidal protein Cbm71 - Clostridium bifermentans
C;Species: Clostridium bifermentans
C;Accession: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
R;Barloy, F.; Delecluse, A.; Nicolas, L.; Decadet, M.M.
A;Title: Cloning and expression of the first anaerobic toxin gene from Clostridium bifermentans.
A;Reference number: JG6033; MUID: 96236023; PMID: 8655486
A;Accession: JG6033
A;Molecule type: DNA
A;Residues: 1-613 <BAR>
A;Cross-references: UNIPROT:Q45882; EMBL:X94146; NID:91246431; PIDN:CAA63860.1; PID:9124

Qy 70 ISVVGQITLGWGVPFAGALTSPYQSFNLTINP-----SDADPMKAFAQMVEVILIDK 120
Db 77 ISLGF1-----PGAEAVPFTINMVFDFWWPKLFGANTEGKDQQLNAINMAVNKNVDN 130

Qy 121 KIEEYAKSKAKAELQLONNFEDYVVALN-----SWKETPLSLRS--KRSQ 164
Db 131 KPLSYNLSNLNTLNKTCIEGLQNLGLFQNAIQVALCQGSTPERVNDQNCPCNPNQPCCKDL 190

Qy	165	DRIELPSQAESHFRNSMSPF-----AVSKFE----VLFPLTYAQAAANTHLLKKDA	212	Db	50	VAPVVGTVSSFUKKGSLLKRLSELWGLIFFPSGSTNLIMODLR-----	95
Db	191	DRASRPTDANSPTQHPEFKRNPWSDENSTOKRTSVELTLPMTTVAATHLLLYEGY	250	Qy	112	AQEVILDKKIEEYAKSKALAELOGIQLNNFEDY---VNAILN-SWFKTPPLSLRSKRSQDR	166
Qy	213	QYFGEENGGYSSSEDAEFTYHQLKLTQQYTDHCYN-----WYNGLNGLGRGSTDWY	264	Db	96	-ETEQFLINQRINTDTIARVNELIGQANREFPQVDFNLPNTQPVPLSTS-SVNT	152
Db	251	IEPMTKWNFHNEQ---YLNLUKVELQOLIHSYSETVRTSFLQFLPLNRSKSSTNA-	304	Qy	167	IRELPSQAESHFRNSMSPFAYSKFEVFLPTYAQAAANTHLLKKDAQVFGEWGYSEDV	226
Qy	265	KPNFRFEMTLYLVLFLIVLPPFDYRILSYKGVTTELTDIFDPFLSLNTQBYGPTFLS	324	Db	153	MQOL-----FLNRLPQFQIQQYQLLPLFAQANMHSFIRDILNADEWGIATL	205
Db	305	-YNRVYRNMTVNCNDIAATWPFEDTHYHQGKLDLTRILSD---TAGFEEYFTG--	357	Qy	227	AEFYHQLKLTOQYTHCUNVYNGLGRGSTDYDWWKFNFRFEMTLYLVLFLWPFPP	286
Qy	325	IENSIRKPHFLDYLQIEBFHTRLQPGFGKDSFNYWSGNYSGNYETRPS---IGSSKTTSPF	381	Db	206	RTYRDYLRLNTYTRDYSNCINTYQTAERGLNTRLHD---MLEFRYTMFLANFEYVSIWSL	261
Db	358	-----DKTSGPB-HSNTP-----NNILDT-PSTYQHSFVSDSIV	392	Qy	287	YDIR-----LYSGKVKBLTRD1-----FTPIFSIANT---LQEYQGPTFLIENS	328
Qy	382	YGDKSTEPVQKLSFDGQKVYRTIANTDVAWPNKGKVYLGVTKVDFSOYDQKNE---TS	437	Db	262	FKYQSLMVSQSGANLYTASGSQFQQTQFTAQNWPFLYSLFQVNSNTYLSGSGTRLSI--	318
Db	393	YSRKELQODIATYS-----TNNSNNCHPYG---LRLSFTGDSRYDGDQNQDPFTTS	441	Qy	329	IRKPHFLDYLQGIEFHTRLQPGFGKDSFNYWSGNYSGNYETRPS---IGSSKTTSPFVYGDKSTE	388
Qy	438	TQTYDSKR-----NNGHV-SAQSISDQL-----PPEI	463	Db	319	-----TTPNIGL-----PGSTTHSLSMSARVNT-----SGGVSSGLIGTGNLN	357
Db	442	NNYCHNSYTAPLITLYNARHLYNAKGSQNLQNEVSLVNTVNGSGSCTCDAWINLYLRRPQT	501	Qy	389	PVQKLSFDGOKVYRTIANTDVAWPNKGKVYLGVTKVDFSOYDQKNE---TSQYDSKRNNG	448
Qy	464	T-----DEPLEXAHSIOLNTAECFLMQRRTIPFPTWTHRSVDFENTI	507	Db	358	H---NFNCSTVLPPLPSTPPVRSWLP-----GTDREGVATSTNWQTE-SFOTTLSLR-CG	407
Db	502	SKNESRPDQKINVLYLPIPETVNGTGGNGLGVISAYPME--LVP-----ENV	547	Qy	449	HVSQAQSIDQLPP---ETTDDEPL---EKAYSHQHLYNAECPLMQDERGT---IPPTWT	497
Qy	508	-DAEKITOLPV--VKAYALSSGASLIEBGPQFT-----GGNLLFLKESSNSIAKFKVTL	557	Db	408	AFSARGNSNTYFPDFYFIRNISGVPLVNRNEDTRPLHYQNIRNIESSGTPGGARAYLVSV	467
Db	548	GDVNADTPKLPLTQKGPFPEKYGSEYNRNLISLREVNNGNNA--VRLSNSQSVGQITN	605	Qy	498	HRSVDFENTIDA-----ERITQLPVVKRAYAL---SSGASIIIEGPFTGCGNLL	541
Qy	558	NSAALLQYRYRIRYASTNTNLRLPVQNSNNDLFLVYTKNTKANKKDDLTQYQFDLATTNS	617	Db	468	HNRK---NNIYAENGTMHHLAEPDTGFTISPIHATQVNQNQTRTIFSEKFGNQODSLR	524
Db	606	QTK---QKYEYCRYAS-----KGDNN---VYFNVDLSENPFNNSFVG-STEESV	649	Qy	542	FLKESSNSIAKFKVTLNSAALLQYRYRIRYASTNTNLRLPVQNSNNDLFLVYTKNTKANKK	601
Qy	618	MGFSDKNELI-----IGAESF--VSNE---KLYIDKIEFIP	649	Db	525	F--EQNTTARYTLRENG---NSNTNLYLRVSIGNTIRVTINGRVTYNSVNNTTNND	578
Db	650	VGVQGENGKYILKLSITTVIPAGSFYVHTNGSSDULFDLRIEFVP	695	Qy	602	-----DDLTYQFDL-ATTNSNMGFSGDKNELIIGAESFVSNEKIV	641
				Db	579	GVNDNGARFSDFNINIGNIVASDNTNTVLDINTVNLNSCTPFD-----	618
				Qy	642	IDKIBP1PVQL	652
				Db	619	LMNIMMVPPTNL	629
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						C:Accession: 13-Jul-1989 #sequence_change 09-Jul-2004	
						R:Widner, W.R.; Whitley, H.R.	
						R: Bacteriol. 171, 965-974, 1989	
						A:Residues: 1-633 <WID>	
						A:Cross-references: UNIPROT:P21253	
						R:Donovan, W.P.; Dankocsik, C.C.; Gilbert, M.P.; Gavron-Burke, M.C.; Carlt	
						C:Accession: A32053; MUID:89123178; PMID:2914879	
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						Mol. Microbiol. 4, 2087-2094, 1990	
						A:Title: Activation of a cryptic crystal protein gene of <i>Bacillus thuringiensis</i> subspeci	
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 Best Local Similarity 19.5%; Pred. No 6.1e-08;
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Qy 295 GVKFBLTRDI-----FTDPIFSANT----LOEYGPFLSIENSTRKPHIF-- 335
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Qy 463 TTDEPLEKAYSHOLNYAECFLMQRRTGTFWTHRSVDFENTIDAERKITOLPVVKAYA 522
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Qy 581 FVQN-----SNNDFLVITYNKTMKDDDLTYQTFDLATTN 615
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 Job time : 65 secs

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